

**WEST**[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 10 of 16 returned.****1. Document ID: US 20020040490 A1**

L1: Entry 1 of 16

File: PGPB

Apr 4, 2002

PGPUB-DOCUMENT-NUMBER: 20020040490

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020040490 A1

TITLE: Expressed sequences of arabidopsis thaliana

PUBLICATION-DATE: April 4, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Gorlach, Jorn	Durham	NC	US	
An, Yong-Qiang	San Diego	CA	US	
Hamilton, Carol M.	Apex	NC	US	
Price, Jennifer L.	Raleigh	NC	US	
Paines, Tracy M.	Durham	NC	US	
Yu, Yang	Martinsville	NJ	US	
Fameaka, Joshua G.	Durham	NC	US	
Page, Amy	Durham	NC	US	
Mathew, Abraham V.	Cary	NC	US	
Ledford, Brooke L.	Holly Springs	NC	US	
Woesner, Jeffrey P.	Hillsborough	NC	US	
Haas, William David	Durham	NC	US	
Garcia, Carlos A.	Carrboro	NC	US	
Kricker, Maja	Pittsboro	NC	US	
Slater, Ted	Apex	NC	US	
Davis, Keith R.	Durham	NC	US	
Allen, Keith	Cary	NC	US	
Hoffman, Neil	Chapel Hill	NC	US	
Hurban, Patrick	Raleigh	NC	US	

US CL-CURRENT: 800/288; 435/4, 536/23\_2, 536/23.6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMPC
<a href="#">Draw</a>	<a href="#">Desc</a>	<a href="#">Image</a>									

**2. Document ID: US 20020040489 A1**

L1: Entry 2 of 16

File: PGPB

Apr 4, 2002

PGPUB-DOCUMENT-NUMBER: 20020040489

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020040489 A1

TITLE: Expressed sequences of arabidopsis thaliana

PUBLICATION-DATE: April 4, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Gorlach, John	Durham	NC	US	
An, Yung-Qiang	San Diego	CA	US	
Hamilton, Carol M.	Apex	NC	US	
Price, Jennifer L.	Raleigh	NC	US	
Paines, Tracy M.	Durham	NC	US	
Yu, Yang	Martinsville	NJ	US	
Rameaka, Joshua G.	Durham	NC	US	
Page, Amy	Durham	NC	US	
Mathew, Abraham V.	Cary	NC	US	
Bedford, Brooke L.	Holly Springs	NC	US	
Woesner, Jeffrey P.	Hillsborough	NC	US	
Haas, William David	Durham	NC	US	
Garcia, Carlos A.	Carrboro	NC	US	
Kricker, Maja	Pittsboro	NC	US	
Slater, Ted	Apex	NC	US	
Davis, Keith R.	Durham	NC	US	
Allen, Keith	Cary	NC	US	
Hoffman, Neil	Chapel Hill	NC	US	
Hurban, Patrick	Raleigh	NC	US	

US-CL-CURFENT: 800/288; 435/4, 536/23.2, 536/23.6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC
<a href="#">Draw Desc</a>	<a href="#">Image</a>										

## 3. Document ID: US 20020023280 A1

L1: Entry 3 of 16

File: PGPB

Feb 21, 2002

F3PUB-DOCUMENT-NUMBER: 20020023280

F3PUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020023280 A1

TITLE: Expressed sequences of arabidopsis thaliana

PUBLICATION-DATE: February 21, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Gorlach, Jorn	Durham	NC	US	
An, Yong-Qiang	San Diego	CA	US	
Hamilton, Carol M.	Apex	NC	US	
Price, Jennifer L.	Raleigh	NC	US	
Raines, Tracy M.	Durham	NC	US	
Yu, Yang	Martinsville	NJ	US	
Rameaka, Joshua G.	Durham	NC	US	
Page, Amy	Durham	NC	US	
Mathew, Abraham V.	Cary	NC	US	
Ledford, Brooke L.	Holly Springs	NC	US	
Woessner, Jeffrey P.	Hillsborough	NC	US	
Haas, William David	Durham	NC	US	
Garcia, Carlos A.	Carrboro	NC	US	
Kricker, Maja	Pittsboro	NC	US	
Slater, Ted	Apex	NC	US	
Davis, Keith R.	Durham	NC	US	
Allen, Keith	Cary	NC	US	
Hoffman, Neil	Chapel Hill	NC	US	
Hurban, Patrick	Raleigh	NC	US	

US-CL-CURRENT: 800/288; 435/4, 536/23.2, 536/23.6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC
Draw	Desc	Image								

4. Document ID: US 20010051335 A1

L1: Entry 4 of 16

File: PGPB

Dec 13, 2001

PGPUB-DOCUMENT-NUMBER: 20010051335  
 PGPUB-FILING-TYPE: new  
 DOCUMENT-IDENTIFIER: US 20010051335 A1

TITLE: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

PUBLICATION-DATE: December 13, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
LALGUDI, RAGHUNATH V.	CLAYTON	MD	US	
ITO, LAURA Y.	PLEASANTON	CA	US	
SHERMAN, BRADLEY K.	OAKLAND	CA	US	

US-CL-CURRENT: 435/6; 435/69.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC
Draw	Desc	Image								

5. Document ID: US 6368848 B1

L1: Entry 5 of 16

File: USPT

US-PAT-NO: 6368848

DOCUMENT-IDENTIFIER: US 6368848 B1

TITLE: Compositions to identify plant proteins that function in G-protein coupled systems

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC	
Draw	Desc	Image									

】 6. Document ID: US 6333403 B1

L1: Entry 6 of 16

File: USPT

US-PAT-NO: 6333403

DOCUMENT-IDENTIFIER: US 6333403 B1

TITLE: Chromosome 17p-linked prostate cancer susceptibility gene and a paralog and orthologous genes

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC	
Draw	Desc	Image									

】 7. Document ID: US 6294348 B1

L1: Entry 7 of 16

File: USPT

US-PAT-NO: 6294348

DOCUMENT-IDENTIFIER: US 6294348 B1

TITLE: TFAF inhibitors

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC	
Draw	Desc	Image									

】 8. Document ID: US 6090784 A

L1: Entry 8 of 16

File: USPT

US-PAT-NO: 6090784

DOCUMENT-IDENTIFIER: US 6090784 A

TITLE: RNA polymerase II peptides and methods of use

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC	
Draw	Desc	Image									

】 9. Document ID: US 6060303 A

L1: Entry 9 of 16

File: USPT

US-PAT-NO: 6060303

DOCUMENT-IDENTIFIER: US 6060303 A

TITLE: TRAF inhibitors

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC
Draw Desc		Image								

10. Document ID: US 6004553 A

L1: Entry 10 of 16

File: USPT

US-PAT-NO: 6004553

DOCUMENT-IDENTIFIER: US 6004553 A

TITLE: TRAF inhibitors

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC
Draw Desc		Image								

Term	Documents
ARABIDOPSIS.DWPI,EPAB,JPAB,USPT,PGPB.	2648
ARABIDOPSI.DWPI,EPAB,JPAB,USPT,PGPB.	3
KINASE.DWPI,EPAB,JPAB,USPT,PGPB.	29622
KINASES.DWPI,EPAB,JPAB,USPT,PGPB.	6986
SHAGGY.DWPI,EPAB,JPAB,USPT,PGPB.	475
SHAGGIES	0
SHAGGYS	0
ASK.DWPI,EPAB,JPAB,USPT,PGPB.	13293
ASKS.DWPI,EPAB,JPAB,USPT,PGPB.	10359
(ARABIDOPSIS AND (SHAGGY OR ASK) AND KINASE).USPT,PGPB,JPAB,EPAB,DWPI.	16
(ARABIDOPSIS AND KINASE AND (SHAGGY OR ASK)).USPT,PGPB,JPAB,EPAB,DWPI.	16

Display Format:

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## Search Results - Record(s) 11 through 16 of 16 returned.

## 11. Document ID: US 5989897 A

L1: Entry 11 of 16

File: USPT

US-PAT-NO: 5989897

DOCUMENT-IDENTIFIER: US 5989897 A

TITLE: Yeast silencing genes proteins and methods

<a href="#">Full</a>	<a href="#">Title</a>	<a href="#">Citation</a>	<a href="#">Front</a>	<a href="#">Review</a>	<a href="#">Classification</a>	<a href="#">Date</a>	<a href="#">Reference</a>	<a href="#">Sequences</a>	<a href="#">Attachments</a>
<a href="#">Draw</a>	<a href="#">Desc</a>	<a href="#">Image</a>							

KMC

## 12. Document ID: US 5985584 A

L1: Entry 12 of 16

File: USPT

US-PAT-NO: 5985584

DOCUMENT-IDENTIFIER: US 5985584 A

TITLE: Method to identify plant proteins that function in G protein coupled systems and compositions therefor

<a href="#">Full</a>	<a href="#">Title</a>	<a href="#">Citation</a>	<a href="#">Front</a>	<a href="#">Review</a>	<a href="#">Classification</a>	<a href="#">Date</a>	<a href="#">Reference</a>	<a href="#">Sequences</a>	<a href="#">Attachments</a>
<a href="#">Draw</a>	<a href="#">Desc</a>	<a href="#">Image</a>							

KMC

## 13. Document ID: US 5789550 A

L1: Entry 13 of 16

File: USPT

US-PAT-NO: 5789550

DOCUMENT-IDENTIFIER: US 5789550 A

TITLE: TRAF inhibitors

<a href="#">Full</a>	<a href="#">Title</a>	<a href="#">Citation</a>	<a href="#">Front</a>	<a href="#">Review</a>	<a href="#">Classification</a>	<a href="#">Date</a>	<a href="#">Reference</a>	<a href="#">Sequences</a>	<a href="#">Attachments</a>
<a href="#">Draw</a>	<a href="#">Desc</a>	<a href="#">Image</a>							

KMC

## 14. Document ID: US 5599670 A

L1: Entry 14 of 16

File: USPT

US-PAT-NO: 5599670

DOCUMENT-IDENTIFIER: US 5599670 A

TITLE:  $\beta$ -glucuronidase and glucuronide permease gene system

<a href="#">Full</a>	<a href="#">Title</a>	<a href="#">Citation</a>	<a href="#">Front</a>	<a href="#">Review</a>	<a href="#">Classification</a>	<a href="#">Date</a>	<a href="#">Reference</a>	<a href="#">Sequences</a>	<a href="#">Attachments</a>	<a href="#">KMC</a>
<a href="#">Draw Desc</a>   <a href="#">Image</a>										

J 15. Document ID: US 5432081 A

L1: Entry 15 of 16

File: USPT

US-PAT-NO: 5432081

DOCUMENT-IDENTIFIER: US 5432081 A

TITLE: Host cells transformed with the *E. coli* glucuronide permease gene

<a href="#">Full</a>	<a href="#">Title</a>	<a href="#">Citation</a>	<a href="#">Front</a>	<a href="#">Review</a>	<a href="#">Classification</a>	<a href="#">Date</a>	<a href="#">Reference</a>	<a href="#">Sequences</a>	<a href="#">Attachments</a>	<a href="#">KMC</a>
<a href="#">Draw Desc</a>   <a href="#">Image</a>										

J 16. Document ID: US 5268463 A

L1: Entry 16 of 16

File: USPT

US-PAT-NO: 5268463

DOCUMENT-IDENTIFIER: US 5268463 A

TITLE: Plant promoter  $\alpha$ -glucuronidase gene construct

<a href="#">Full</a>	<a href="#">Title</a>	<a href="#">Citation</a>	<a href="#">Front</a>	<a href="#">Review</a>	<a href="#">Classification</a>	<a href="#">Date</a>	<a href="#">Reference</a>	<a href="#">Sequences</a>	<a href="#">Attachments</a>	<a href="#">KMC</a>
<a href="#">Draw Desc</a>   <a href="#">Image</a>										

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Term	Documents
ARABIDOPSIS,DWPI,EPAB,JPAB,USPT,PGPB.	2648
ARABIDOPSI,DWPI,EPAB,JPAB,USPT,PGPB.	3
KINASE,DWPI,EPAB,JPAB,USPT,PGPB.	29622
KINASES,DWPI,EPAB,JPAB,USPT,PGPB.	6986
SHAGGY,DWPI,EPAB,JPAB,USPT,PGPB.	475
SHAGGIES	0
SHAGGYS	0
ASK,DWPI,EPAB,JPAB,USPT,PGPB.	13293
ASKS,DWPI,EPAB,JPAB,USPT,PGPB.	10359
(ARABIDOPSIS AND (SHAGGY OR ASK) AND KINASE),USPT,PGPB,JPAB,EPAB,DWPI.	16
(ARABIDOPSIS AND KINASE AND (SHAGGY OR ASK)),USPT,PGPB,JPAB,EPAB,DWPI.	16

Display Format:

[Previous Page](#)      [Next Page](#)

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? s arabidopsis and kinas?  
    95824 ARABILOPSIS  
    903032 KINAS?  
    S1    7347 ARABILOPSIS AND KINAS?  
? s s1 and shaggy  
    "347 S1  
    324 SHAGGY  
    S2    90 S1 AND SHAGGY  
? s s1 and ask  
    "347 S1  
    21678 ASK  
    S3    55 S1 AND ASK  
? s s1 and /zeta  
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? s s1 and ?zeta  
>>>File 155 processing for ?ZETA stopped at ALOGRAFT  
>>>File 5 processing for ?ZETA stopped at ACTIVASTING  
>>>File 6 processing for ?ZETA stopped at AUTOCC  
>>>File 10 processing for ?ZETA stopped at ANIAMA  
>>>File 34 processing for ?ZETA stopped at ADIABATIC MECHANISM      j >  
>>>File 44 processing for ?ZETA stopped at BAHAMA I., FRESH CREEK  
<-----User Break----->  
u'  
? s s1 and dzeta  
    7347 S1  
    214 DZETA  
    S4    0 S1 AND DZETA  
? s s1 and zeta  
    7347 S1  
    40199 ZETA  
    S5    21 S1 AND ZETA  
? rd s2  
>>>Duplicate detection is not supported for File 235.  
>>>Duplicate detection is not supported for File 306.  
>>>Records from unsupported files will be retained in the RD set.  
...examined 50 records (50)  
...completed examining records  
    S6    28 RD S2 (unique items)  
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>>>No matching display code(s) found in file(s): 65, 235, 306
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6,3,AB/1 (Item 1 from file: 155)  
DIALOG(R) File 155: MEDLINE(R)

12927072 21673983 PMID: 11820813  
The **UCU1** **Arabidopsis** gene encodes a **SHAGGY/GSK3-like kinase** required for cel. expansion along the proximodistal axis.  
Perez-Perez Jose Manuel; Ponce Maria Rosa; Micol Jose Luis  
Division de Genetica and Instituto de Biotecnologia, Universidad Miguel Hernandez, Campus de Elche, 03202 Elche, Alicante, Spain.  
Developmental biology (United States) Feb 15 2002, 242 (2) p161-73,  
ISSN 0012-1606 Journal Code: 0372762  
Document type: Journal Article  
Languages: ENGLISH  
Main Citation Owner: NLM  
Record type: Completed  
Most signal transduction pathways central to development are not shared by plants and animals. Such is the case of the Wingless/Wnt signaling pathway, whose components play key roles in metazoan pattern formation and tumorigenesis, but are absent in plants, with the exception of **SHAGGY/GSK3**, a cytoplasmic protein **kinase** represented in the genome of **Arabidopsis thaliana** by a family of 10 AtSK genes for which

mutational evidence is scarce. Here, we describe the characterization of mutant alleles of the **Arabidopsis** ULTRACURVATA1 (UCU1) gene, the two strongest of which dramatically reduce cell expansion along the proximodistal axis, dwarfing the mutant plants, whose cells expand properly across but not along most organs. Proximodistal expansion of adaxial (dorsal) and abaxial (ventral) leaf cells exhibits a differential dependence on UCU1 function, as suggested by the leaves of ucu1 mutants, which are rolled spirally downward in a circinate manner. We have positionally cloned the UCU1 gene, which encodes an AtSK protein involved in the cross-talk between auxin and brassinosteroid signaling pathways, as indicated by the responses of ucu1 mutants to plant hormones and the phenotypes of double mutants involving ucu1 alleles.

6/3,AB/2 (Item 2 from file: 155)  
DIALOG(R)File 155: MEDLINE(R)

12922630 21836537 PMID: 11847343

Regulation of brassinosteroid signaling by a GSK3/**SHAGGY**-like kinase.

Li Jianming; Nam Kyung Hee  
Department of Molecular, Cellular, and Developmental Biology, University of Michigan, Ann Arbor, MI 48109-1048, USA.

Science (United States) Feb 15 2002; 295 (5558) p1299-301, ISSN 1095-9203 Journal Code: 0404511

Contract/Grant No.: GM60519; GM; NIGMS  
Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

GSK3/**SHAGGY** is a highly conserved serine/threonine kinase implicated in many signaling pathways in eukaryotes. Although many GSK3/**SHAGGY**-like kinases have been identified in plants, little is known about their functions in plant growth and development. Here we show that the **Arabidopsis** BRASSINOSTEROID-INSENSITIVE 2 (BIN2) gene encodes a GSK3/**SHAGGY**-like kinase. Gain-of-function mutations within its coding sequence or its overexpression inhibit brassinosteroid (BR) signaling, resulting in plants that resemble BR-deficient and BR-response mutants. In contrast, reduced BIN2 expression via cosuppression partially rescues a weak BR-signaling mutation. Thus, BIN2 acts as a negative regulator to control steroid signaling in plants.

6/3,AB/3 (Item 3 from file: 155)  
DIALOG(R)File 155: MEDLINE(R)

12544189 21425095 PMID: 11532176

Constitutive over-expression of AtGSK1 induces NaCl stress responses in the absence of NaCl stress and results in enhanced NaCl tolerance in **Arabidopsis**.

Piao H L; Lim J H; Kim S J; Cheong G W; Hwang I  
Center for Plant Intracellular Trafficking, Pohang University of Science and Technology, Pohang, 790-784, Korea.

Plant journal : for cell and molecular biology (England) Aug 2001; 27 (4) p305-14, ISSN 0960-7412 Journal Code: 9207397

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

GSK3/**shaggy**-like protein kinases have been shown to play diverse roles in development and signal transduction pathways in various organisms. An **Arabidopsis** homologue of GSK3/**shaggy**-like kinase, AtGSK1, has been shown to be involved in NaCl stress responses. In order to further clarify the role of AtGSK1 in NaCl stress

responses in plants, we generated transgenic **Arabidopsis** plants that over-expressed AtGSK1 mRNA. These plants showed enhanced resistance to NaCl stress when assayed either as whole plants or by measurement of root growth on NaCl plates. In addition, AtGSK1 transgenic plants in the absence of NaCl stress showed phenotypic changes, such as accumulation of anthocyanin, that were similar to those observed in wild-type plants under NaCl stress. Transgenic plants accumulated 30-50% more Na<sup>+</sup> than did wild-type plants when subjected to NaCl stress, and Ca<sup>2+</sup> content was increased by 15-30% in the transgenic plants regardless of the NaCl stress level. Northern blotting revealed that AtGSK1 over-expression induced expression of the NaCl stress-responsive genes AtCP1, RD29A and CHS1 in the absence of NaCl stress. In addition, AtCBL1 and AtCP1 were super-induced in the NaCl-stressed transgenic plants. Taken together, these results suggest that AtGSK1 is involved in the signal transduction pathway(s) of NaCl stress responses in **Arabidopsis**.

6/3,AB/4 (Item 4 from file: 155)

DIALOG(R)File 155: MEDLINE(R)

10692632 20223136 PMID: 10758494

**Arabidopsis thaliana SHAGGY-related protein kinases**  
(AtSK11 and 12) function in perianth and gynoecium development.  
Cornelis M C; Van Lammeren A A; Kreis M  
Universite de Paris-Sud, Institut de Biotechnologie des Plantes (IBP),  
UMR/CNRS 8618, Batiment 630, F-91405 Orsay Cedex, France.

Plant journal : for cell and molecular biology (ENGLAND) Mar 2000, 21  
(5) p419-29, ISSN 0960-7412 Journal Code: 9207397

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

In higher plants, the correct patterning of the floral meristem in terms of organ type, number and form is the result of a concerted expression of a network of genes. We describe phenotypes of flower patterning, resulting from a reduction of transcript levels of the **Arabidopsis SHAGGY**-related protein kinase genes AtSK11(ASKalpha) and AtSK12(ASKgamma). The AtSK genes are plant homologues of the *Drosophila shaggy* (SGG) gene and the mammalian Glycogen-Synthase Kinase-3 (GSK-3). The SGG protein kinase is a key component of the wingless signalling pathway and is required for the establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11(ASKalpha) and AtSK12(ASKgamma) genes during wild-type **Arabidopsis** inflorescence development, detected by in situ hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11(ASKalpha) and AtSK12(ASKgamma) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11(ASKalpha) and AtSK12(ASKgamma) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the apical-basal patterning of the gynoecium.

6/3,AB/5 (Item 5 from file. 155)

DIALOG(R)File 155: MEDLINE(R)

10209761 99214484 PMID: 10198112

An **Arabidopsis** GSK3/shaggy-like gene that complements yeast salt stress-sensitive mutants is induced by NaCl and abscisic acid.  
Piao H L; Pih K T; Lim J H; Kang S G; Jin J B; Kim S H; Hwang I  
Department of Molecular Biology, Biotechnology Research Center,  
Gyeongsang National University, Chinju, 660-701, Korea.

Plant physiology (UNITED STATES) Apr 1999, 119 (4) p1527-34, ISSN 0032-0889 Journal Code: C401224

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

**GSK3/shaggy-like** genes encode **kinases** that are involved in a variety of biological processes. By functional complementation of the yeast calcineurin mutant strain DHT22-1a with a NaCl stress-sensitive phenotype, we isolated the **Arabidopsis** cDNA AtGSK1, which encodes a GSK3/**shaggy-like** protein **kinase**. AtGSK1 rescued the yeast calcineurin mutant cells from the effects of high NaCl. Also, the AtGSK1 gene turned on the transcription of the NaCl stress-inducible PMR2A gene in the calcineurin mutant cells under NaCl stress. To further define the role of AtGSK1 in the yeast cells we introduced a deletion mutation at the MCK1 gene, a yeast homolog of GSK3, and examined the phenotype of the mutant. The mck1 mutant exhibited a NaCl stress-sensitive phenotype that was rescued by AtGSK1. Also, constitutive expression of MCK1 complemented the NaCl-sensitive phenotype of the calcineurin mutants. Therefore, these results suggest that Mck1p is involved in the NaCl stress signalling in yeast and that AtGSK1 may functionally replace Mck1p in the NaCl stress response in the calcineurin mutant. To investigate the biological function of AtGSK1 in **Arabidopsis** we examined the expression of AtGSK1. Northern-blot analysis revealed that the expression is differentially regulated in various tissues with a high level expression in flower tissues. In addition, the AtGSK1 expression was induced by NaCl and exogenously applied ABA but not by KCl. Taken together, these results suggest that AtGSK1 is involved in the osmotic stress response in **Arabidopsis**.

6/3,AB/6 (Item 6 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)

10185524 99178301 PMID: 10080716

Characterization of three novel members of the **Arabidopsis SHAGGY**-related protein **kinase** (ASK) multigene family.

Bornelas M C; Wittich P; von Recklinghausen I; van Lammeren A; Kreis M  
Institut de Biotechnologie des Plantes EFS/CNRS 569, Universite de Paris-Sud, Orsay, France.

Plant molecular biology (NETHERLANDS) Jan 1999, 39 (1) p137-47,

ISSN 0167-4412 Journal Code: 9106343

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

In this paper we report the characterization of three novel members of the **Arabidopsis shaggy-related protein kinase** (ASK) multigene family, named **ASKdzeta** (ASKzeta), **ASKetha** (ASKeta) and **ASKiota** (ASKiota). The proteins encoded by the ASK genes share a highly conserved catalytic protein **kinase** domain and show about 70% identity to **SHAGGY** (SGG) and glycogen synthase **kinase** -3 (GSK-3) from *Drosophila* and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in *Drosophila*. At least ten different ASK genes are expected to be present per haploid genome of *A. thaliana*. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein **kinases** demonstrated a clear distinction between the plant and the animal **kinases**. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect

biochemical and/or biological properties of these **kinases**. The differential expression patterns of five ASK genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While ASKzeta is expressed in the whole embryo during its development, ASKeta expression is limited to the suspensor cells. No signal was detected for ASKalpha, ASKgamma and ASKiota in developing embryos.

6,3,AB/7 (Item 7 from file: 155)  
DIALOG(R)File 155: MEDLINE(R)

10039177 99023747 PMID: 9804971

An evolutionary conserved group of plant GSK-3/**shaggy**-like protein **kinase** genes preferentially expressed in developing pollen.

Ticatinsky G; Tavares R; Takvorian A; Schwebel-Dugue N; Twell D; Kreis M  
Institut de Biotechnologie des Plantes, Laboratoire de Biologie du  
Developpement des Plantes, Batiment 630, Universite de Paris-Sud CNRS/ERS  
569, F-91405 Orsay Cedex, France.

Biochimica et biophysica acta (NETHERLANDS) Nov 8 1998, 1442 (2-3)  
p261-73, ISSN 0006-3002 Journal Code: 0217513

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Genes and cDNAs encoding plant protein **kinases** highly homologous to the animal GSK-3/**shaggy** subfamily were isolated from **Arabidopsis thaliana**, *Brassica napus*, *Petunia hybrida* and *Nicotiana tabacum* using the *P. hybrida* PSK6 GSK-3/**shaggy** related cDNA as a probe. All the derived protein sequences contained the characteristic catalytic domain of GSK-3/**shaggy** protein **kinases**. Sequence comparisons within the catalytic domain with other plant GSK-3/**shaggy** like **kinases** clearly indicate that the novel sequences form an isolated group of genes termed the PSK6 group. All the proteins within this group possess an amino-terminal extension which contains short amino acid motifs highly conserved between species and possibly implicated in mitochondrial targeting. Northern hybridisation experiments and reverse transcriptase PCR analysis demonstrated that these novel cDNAs are predominantly expressed in developing pollen. The three genes isolated from *P. hybrida* and *A. thaliana* show the same genomic organisation into 12 introns and 13 exons. Although the size of the introns varies, their positions are conserved between genes and species. The comparison of these gene structures and the analysis of deduced protein sequences belonging to different plants hold important information to understand the function of individual members. They suggest that some of the characterised sequences represent most likely true orthologues whereas others must be paralogues. They also allow us to discuss the evolution of the plant GSK-3/**shaggy** like gene family with regard to plant speciation.

6,3,AB/8 (Item 8 from file: 155)  
DIALOG(R)File 155: MEDLINE(R)

09842008 98278841 PMID: 9611268

The **Arabidopsis SHAGGY**-related protein **kinase** (ASK) gene family: structure, organization and evolution.

D'Innelas M C; Lejeune B; Dron M; Kreis M

Institut de Biotechnologie des Plantes, ERS/CNRS 569, Universite de Paris-Sud, Batiment 630, F-91405, Orsay, Cedex, France.

Gene (NETHERLANDS) Jun 8 1998, 212 (2) p249-57, ISSN 0378-1119  
Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Higher plants contain a multigene family encoding proteins that share a highly conserved catalytic protein **kinase** domain about 70% identical to **SHAGGY** protein **kinase** (SGG) and glycogen synthase **kinase**-3 (GSK-3), respectively, from *Drosophila* and mammals. In this study we have characterized the structure and evolution of the *Arabidopsis* **SHAGGY**-related protein **kinase** (ASK) gene family. At least ten ASK genes are present per haploid genome of *Arabidopsis*. The genomic sequences of five ASK genes show a strikingly high conservation of intron positions and exon lengths. Phylogenetic analyses suggested that the *Arabidopsis* gene family contains at least three ancient classes of genes that diverged early in land plant evolution. The different classes may reflect specificity of substrates and/or biological functions. Eight out of the ten predicted ASK genes were mapped and shown to be dispersed over the five *Arabidopsis* chromosomes. A tentative model for the organization and evolution of the *Arabidopsis* ASK genes is presented.

6/3,AB/9 (Item 9 from file: 155)  
DIALOG(R)File 155: MEDLINE(R)

08425409 95178552 PMID: 7873606

Isolation and expression during pollen development of a tobacco cDNA clone encoding a protein **kinase** homologous to **shaggy/glycogen synthase kinase-3**.

Einzenberger E; Eller N; Heberle-Bors E; Vicente O  
Institute of Microbiology and Genetics, University of Vienna, Austria.  
Biochimica et biophysica acta (NETHERLANDS) Feb 21 1995, 1260 (3)  
p315-9, ISSN 0006-3002 Journal Code: 0217513

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We have isolated a tobacco (*Nicotiana tabacum* L.) cDNA clone encoding a putative serine/threonine protein **kinase**, which shows highest homology to previously described families of alfalfa and *Arabidopsis* protein **kinases** and to their homologues rat glycogen synthase **kinase**-3 and *Drosophila* **shaggy kinases**. Northern experiments showed that NtK-4 is expressed in all sporophytic tobacco tissues tested, as well as in gametophytic and embryogenic pollen.

6/3,AB/10 (Item 10 from file: 155)  
DIALOG(R)File 155: MEDLINE(R)

08422393 95170005 PMID: 7865793

Inflorescence-specific expression of AtK-1, a novel *Arabidopsis* thaliana homologue of **shaggy/glycogen synthase kinase-3**.

Jonak C; Heberle-Bors E; Hirt H  
Institute of Microbiology and Genetics, University of Vienna, Vienna Biocenter, Austria.

Plant molecular biology (NETHERLANDS) Jan 1995, 27 (1) p217-21,  
ISSN 0167-4412 Journal Code: 9106343

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We report here the isolation of the *Arabidopsis* thaliana gene AtK-1. The predicted protein sequence of AtK-1 shows 70% identity to the *Arabidopsis* ASK and alfalfa MsK **kinases** that are homologs of the *Drosophila* **shaggy** and rat GSK-3 serine/threonine protein **kinases** playing an important role in signal transduction processes in animals. Northern analysis of different organs revealed exclusive expression in inflorescences suggesting an involvement of the AtK-1

kinase in reproduction-specific processes.

6/3,AB/11 (Item 11 from file: 155)  
DIALOG(R) File 155: MEDLINE(R)

08026635 94150468 PMID: 7509023

**Arabidopsis** homologs of the **shaggy** and GSK-3 protein kinases : molecular cloning and functional expression in *Escherichia coli*.

Bianchi M W; Guivarc'h D; Thomas M; Woodgett J R; Kreis M  
Centre de Recherches sur les Plantes URA 1128, Universite de Paris-Sud,  
Orsay, France.

Molecular & general genetics : MGG (GERMANY) Feb 1994, 242 (3)  
p337-45, ISSN 0026-8925 Journal Code: 0125036

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The conservation in evolution of fundamental signal transduction modules offers a means of isolating genes likely to be involved in plant development. We have amplified by PCR **Arabidopsis** cDNA and genomic sequences related to the product of the **shaggy/zeste-white 3** (sgg) segment polarity gene of *Drosophila*. This regulatory protein is functionally homologous to glycogen synthase **kinase-3** in mammals (GSK-3), which regulates, among others, the DNA-binding activity of the c-jun/AP1 transcription factor. Analysis of PCR products led to the identification of five genes; for two of which, corresponding full-length cDNAs, ASK-alpha and gamma (for **Arabidopsis shaggy**-related protein **kinase**), were characterized. The encoded proteins were 70% identical to GSK-3 and sgg over the protein **kinase** catalytic domain and, after production in *Escherichia coli*, autophosphorylated mainly on threonine and serine residues, but phosphotyrosine was also detected. ASK-alpha and ASK-gamma also phosphorylated phosphatase inhibitor-2 and myelin basic protein, on threonine and serine, respectively. The high conservation of the protein **kinases** of GSK-3 family, and their action at the transcriptional level, suggest that the ASK proteins have important functions in higher plants.

6/3,AB/12 (Item 1 from file: 5)  
DIALOG(R) File 5: Biosis Previews(R)  
(c) 2002 BIOSIS. All rts. reserv.

13554801 BIOSIS NO.: 200200183622

Non-purified anti-peptide sera generate tissue specific artefacts in immunohistochemical staining of **Arabidopsis thaliana**.

AUTHOR: Tavares R; Vidal J; van Lammeren A; Kreis M(a)

AUTHOR ADDRESS: (a) Institut de Biotechnologie des Plantes (IBP), Universite de Paris-Sud, UMR CNRS 8618, Batiment 530, 91405, Orsay Cedex\*\*France

E-Mail: kreis@ibp.u-psud.fr

JOURNAL: Plant Science (Shannon) 162 (2):p309-314 February, 2002

MEDIUM: print

ISSN: 0168-9452

DOCUMENT TYPE: Article

REJOINED TYPE: Abstract

LANGUAGE: English

ABSTRACT: Polyclonal antibodies raised against short synthetic peptides require coupling of the peptide to a larger carrier molecule before immunisation. A significant fraction of the total antibody pool of the serum from the immunised animal corresponds to carrier-specific antibodies, which may generate tissue specific artefacts not detected with the pre-immune sera. Using four non-purified anti-peptide sera,

corresponding to specific amino-terminal domains of four different *Arabidopsis thaliana* **SHAGGY** like **kinases** (AtSKs), we demonstrated that the obtained immunohistochemical staining patterns are not related to the peptide specific antibodies. The purification of the anti-peptide antibodies allowed the elimination of the artefactual tissue specific labelling, and revealed a completely different protein localisation. Hence, removal of non-specific antibodies from the immune serum is essential when performing immunohistochemical studies.

2002

6/3,AB/13 (Item 2 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
(c) 2002 BIOSIS. All rts. reserv.

09606211 BIOSIS NO.: 199598061129  
**Arabidopsis** homologues of the **shaggy**/GSK-3 protein **kinase**

AUTHOR: Bianchi Michele W; Guivarc'h Dominique; Kreis Martin  
AUTHOR ADDRESS: Biologie Developpement Plantes, Bat. 430, Univ. Paris-Sud,  
F-91405 Orsay Cedex\*\*France  
JOURNAL: Acta Botanica Gallica 140 (6):p708  
CONFERENCE/MEETING: Meeting of the Botanical Society of France on the  
Molecular and Cellular Bases of Morphogenesis in Plants Paris, France  
December 5, 1992  
RECORD TYPE: Citation  
LANGUAGE: English

6/3,AB/14 (Item 1 from file: 10)  
DIALOG(R)File 10:AGRICOLA  
(c) format only 2002 The Dialog Corporation. All rts. reserv.

3971423 23240936 Holding Library: AGL  
Constitutive over-expression of AtGSK1 induces NaCl stress responses in  
the absence of NaCl stress and results in enhanced NaCl tolerance in  
**Arabidopsis**  
Piao, H.L. Lim, J.H.; Kim, S.J.; Cheong, G.W.; Hwang, I.  
Oxford : Blackwell Sciences Ltd.  
The Plant journal : for cell and molecular biology. Aug 2001. v. 27 (4)  
p. 305-314.

ISSN: 0960-7412  
DNAL CALL NO: QK710.P68  
Language: English  
GSK3/**shaggy**-like protein **kinases** have been shown to play  
diverse roles in development and signal transduction pathways in various  
organisms. An **Arabidopsis** homologue of GSK3/**shaggy**-like  
**kinase**, AtGSK1, has been shown to be involved in NaCl stress  
responses. In order to further clarify the role of AtGSK1 in NaCl stress  
responses in plants, we generated transgenic **Arabidopsis** plants that  
over-expressed AtGSK1 mRNA. These plants showed enhanced resistance to NaCl  
stress when assayed either as whole plants or by measurement of root growth  
on NaCl plates. In addition, AtGSK1 transgenic plants in the absence of  
NaCl stress showed phenotypic changes, such as accumulation of anthocyanin,  
that were similar to those observed in wild-type plants under NaCl stress.  
Transgenic plants accumulated 30-50% more Na<sup>+</sup> than did wild-type plants  
when subjected to NaCl stress, and Ca(2+) content was increased by 15-30%  
in the transgenic plants regardless of the NaCl stress level. Northern  
blotting revealed that AtGSK1 over-expression induced expression of the  
NaCl stress-responsive genes AtCP1, RD29A and CHS1 in the absence of NaCl  
stress. In addition, AtCBL1 and AtCP1 were super-induced in the  
NaCl-stressed transgenic plants. Taken together, these results suggest that  
AtGSK1 is involved in the signal transduction pathway(s) of NaCl stress

responses in **Arabidopsis**.

6/3,AB/15 (Item 2 from file: 10)  
DIALOG(R)File 10:AGRICOLA  
(c) format only 2002 The Dialog Corporation. All rts. reserv.

3417520 20438255 Holding Library: AGL  
Plant genes encoding homologues of the SNF1 and **shaggy** protein

**kinases**

Kreis, M. Bianchi, M.W.; Ferrant, V.; Le Guen, L.; Thomas, M.; Halford, N.G.; Barker, J.H.A.; Hannappel, U.; Vicente-Carabajosa, J.; Shewry, P.R.

Universite Paris-XI, Orsay, Fr.

[Berlin ; New York : Springer-Verlag, c1986-

NATO ASI series. Series H, Cell biology. 1994. v. 81 p. 453-467.

ISSN: 1010-8793 CODEN: NASBE4

DNAL CALL NO: QH573.N37

Language: English

6/3,AB/16 (Item 1 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

10777729 Genuine Article#: 567BM Number of References: 54

Title: AtSK theta, a plant homologue of SGG/GSK-3 marks developing tissues in **Arabidopsis** thaliana (ABSTRACT AVAILABLE)

Author(s): Tavares P; Vidal J; van Lammeren A; Kreis M (REPRINT)

Corporate Source: Univ Paris 11,CNRS, UMR 8618, Lab Biol Dev Plant, Inst Biotechnol Plantes,F-91405 Orsay//France/ (REPRINT); Univ Paris 11,CNRS , UMR 8618, Lab Biol Dev Plant,Inst Biotechnol Plantes,F-91405 Orsay//France//; Wageningen Univ,Lab Plant Cell Biol,NL-6703 BD Wageningen//Netherlands/

Journal: PLANT MOLECULAR BIOLOGY, 2002/ V50, N2 (SEP), P261-271

ISSN: 0167-4412 Publication date: 20020900

Publisher: KLUWER ACADEMIC PUBL, VAN GODEWIJCKSTRAAT 30, 3311 GZ DORDRECHT, NETHERLANDS

Language: English Document Type: ARTICLE

Abstract: The **Arabidopsis** thaliana AtSK sub-family of serine threonine protein **kinases** groups 10 homologues of **SHAGGY** /GSK-3. Previous results obtained with different plant members of the **SHAGGY**/GSK-3 family strongly suggest that these proteins are involved in cell differentiation and stress responses. In order to gain further insight into the biological functions of this family in **A. thaliana**, polyclonal antibodies were raised against specific domains of the AtSKtheta protein. The antibodies were purified and used in immunolocalization studies in various tissues of **A. thaliana**. Our results show that the protein is located in the cell nuclei of various developing organs. Differential protein localization profiles were found in some of the observed tissues, notably during gametophyte and embryo development. Based on this protein location pattern, and on what is known about the mammalian members of the GSK-3 family, we suggest that AtSKtheta may have a role in the regulation of transcription factors.

6/3,AB/17 (Item 2 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

10607229 Genuine Article#: 546ZU Number of References: 14

Title: Single-embryo RT-PCR assay to study gene expression dynamics during embryogenesis in **Arabidopsis** thaliana (ABSTRACT AVAILABLE)

Author(s): Zou JW; Sun MX (REPRINT) ; Yang HY  
Corporate Source: Wuhan Univ, Key Lab MOE Plant Dev Biol, Wuhan  
430072/ Peoples R China/ (REPRINT); Wuhan Univ, Key Lab MOE Plant Dev  
Biol, Wuhan 430072/ Peoples R China/  
Journal: PLANT MOLECULAR BIOLOGY REPORTER, 2002, V20, N1 (MAR), P19-26  
ISSN: 0135-9640 Publication date: 20020300  
Publisher: INT SOC PLANT MOLECULAR BIOLOGY, UNIV GEORGIA, DEPT  
BIOCHEMISTRY, ATHENS, GA 30602 USA  
Language: English Document Type: ARTICLE  
Abstract: We have developed a single-embryo RT-PCR protocol for studying gene expression during plant embryogenesis. Four genes, glyceraldehyde-3 phosphate dehydrogenase (GAPC), shoot-meristemless (STM), monopteros (MP), and shaggy-like kinase etha (ASKeta), from *Arabidopsis thaliana* were used to test the sensitivity and reliability of this method by analyzing the differential signal intensities of their RT-PCR products. The method could detect genes expressed during embryogenesis at a single-embryo level and, therefore, can be used to identify phenotypes. When *in vitro*, embryogenesis also is used to control the time course of zygote development exactly. The single-embryo RT-PCR protocol becomes a powerful method to survey the dynamics of specific gene expression.

6/3/AB 16 (Item 3 from file: 34)  
DIALOG(R)File 34:SciSearch.R Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

10266684 Genuine Article#: 504NE Number of References: 79  
Title: The role of protein **kinases** in the regulation of plant growth and development (ABSTRACT AVAILABLE)  
Author(s): Laurie S; Halford NG (REPRINT)  
Corporate Source: Univ Bristol, Dept Agr Sci, IACR Long Ashton Res Stn, Bristol BS41 9AF/Avon/England/ (REPRINT); Univ Bristol, Dept Agr Sci, IACR Long Ashton Res Stn, Bristol BS41 9AF/Avon/England/  
Journal: PLANT GROWTH REGULATION, 2001, V34, N3 (JUL), P253-265  
ISSN: 0167-4903 Publication date: 20010700  
Publisher: KLUWER ACADEMIC PUBL, VAN GODEWIJKSTRAAT 30, 3311 GZ DORDRECHT, NETHERLANDS  
Language: English Document Type: ARTICLE  
Abstract: We review the role of protein **kinases** in plant hormone-mediated signalling, nutrient signalling and cell cycle control and in the crosstalk between these different contributors to plant growth regulation. The areas of hormone mediated signalling covered include ABA-mediated responses to osmotic stress, wounding and pathogen attack, as well as ethylene and cytokinin signalling pathways. These areas involve members of several major protein **kinase** families, including the SNF1-related protein **kinase**-2 (SnRK2) subfamily, the calcium-dependent protein **kinase** (CDPK) family, the mitogen activated protein (MAP) **kinase** family, the glycogen synthase **kinase** (GSK)-3 'shaggy' family and the receptor-like protein **kinase** (PPK) family. In the section on nutrient signalling we review the role of SnRK1 protein **kinases** in the global regulation of carbon metabolism, including aspects of sugar sensing and assimilate partitioning, and what is known about nitrogen and sulphur nutrient signalling. In the cell cycle section, we summarise progress in the elucidation of cell cycle control systems in plants and discuss the interaction between cell cycle control and development. We expand further on the hypothesis of crosstalk between different signalling pathways in a separate section in which we discuss evidence for interaction between plant growth regulators and the cell cycle, between different nutrient signalling pathways, between nutrient and cell cycle signalling and between nutrient and ABA signalling.

6/3,AB/19 (Item 4 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2001 Inst for Sci Info. All rts. reserv.

09962873 Genuine Article#: 470HZ Number of References: 9  
Title: ULTRACURVATAL, a SHAGGY-like **Arabidopsis** gene required  
for cell elongation (ABSTRACT AVAILABLE)  
Author(s): Perez Pérez JM; Ponce MR; Micol JL (REPRINT)  
Corporate Source: Univ Miguel Hernandez,Div Genet,Campus Elche/Alicante  
03202/Spain/ (REPRINT); Univ Miguel Hernandez,Div Genet,Alicante  
03202/Spain/; Univ Miguel Hernandez,Inst Bioingn,Alicante  
03202/Spain/  
Journal: INTERNATIONAL JOURNAL OF DEVELOPMENTAL BIOLOGY, 2001, V45, 1, P  
S51-S52  
ISSN: 0214-6282 Publication date: 20010000  
Publisher: U E C PRESS, UNIV BASQUE COUNTRY, EDITORIAL SERVICES, PO BOX  
1397, E-48080 BILBAO, SPAIN  
Language: English Document Type: ARTICLE  
Abstract: To better understand the genetic mechanisms underlying plant leaf  
development, we have performed a large-scale screening for  
**Arabidopsis thaliana** mutants to identify those displaying  
abnormally shaped or sized leaves. One of the stronger mutant  
phenotypes found was that of the ultracurvatal ('cul1') mutants, whose  
vegetative and cauline leaves are spirally rolled downwards and show a  
reduced expansion along the longitudinal axis, in contrast to wild type  
leaves, which are flattened organs. We have identified one recessive  
and two semidominant 'cul1' alleles, the most extreme of which cause  
severe dwarfism and a constitutive photomorphogenic response. Following  
a map-based strategy, we have cloned the 'UCU1' gene, which was found to  
encode an intracellular kinase closely related to **SHAGGY**,  
one of the components of the Wingless/Wnt animal signalling pathway.  
The responses of 'cul1' mutants to exogenous plant hormones and the  
genetic analyses of double mutants involving 'cul1' alleles indicate that  
'UCU1' is a key component in several signalling pathways controlling cell  
expansion and overall plant growth, including those of auxins and  
brassinosteroids.

6/3,AB/20 (Item 5 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

04112144 Genuine Article#: RF014 Number of References: 52  
Title: PETUNIA-HYBRIDA HOMOLOGS OF SHAGGY ZESTE-WHITE-3 EXPRESSED IN  
FEMALE AND MALE REPRODUCTIVE-ORGANS (Abstract Available)  
Author(s): DECROOCQFERRANT V; VANDET J; BIANCHI MW; DEVRIES SC; KREIS M  
Corporate Source: UNIV PARIS 11,INST BIOTECHNOL PLANTES,CNRS,URA  
1128,BATIMENT 630/F-91405 ORSAY/FRANCE/; UNIV PARIS 11,INST BIOTECHNOL  
PLANTES,CNRS,URA 1128/F-91405 ORSAY/FRANCE/; AGR UNIV WAGENINGEN,DEPT  
PLANT CYTOL & MORPHOL/6703 BD WAGENINGEN/NETHERLANDS/; AGR UNIV  
WAGENINGEN,DEPT MOLEC BIOL 6703 HA WAGENINGEN/NETHERLANDS/  
Journal: PLANT JOURNAL, 1995, V7, N6 (JUN), P897-911  
ISSN: 0960 7412  
Language: ENGLISH Document Type: ARTICLE  
Abstract: Petunia hybrida ovule-specific cDNA libraries were screened for  
genes encoding homologues of protein **kinases** known to be involved  
in developmental processes. Two cDNAs, PSK4 and PSK6 (Petunia hybrida  
**shaggy** related protein **kinase**), homologous to GSK-3 from  
rat, MDS1 from yeast and to the segment polarity gene **shaggy**  
(zeste white 3 (sgg/zw3) from *Drosophila* were characterized in detail.  
Southern blot analysis showed that the PSK4 and PSK6 genes belong to a  
small multigene family in *P. hybrida*. The PSK4 and PSK6 proteins, which  
are 70% identical to sgg/zw3 and its functional homologue GSK-3 over  
the protein **kinase** catalytic domain and 55% identical to MDS1,

represent two different subgroups of protein **kinases**. RNA gel blot and RT-PCR analyses revealed that the PSK4 gene is expressed during the vegetative phase and the female reproductive phase of development and the PSK6 gene predominantly during the male and female reproductive phases. *In situ* hybridization on developing flower buds confirmed that PSK4 is expressed throughout the different developmental stages from ovule primordium formation until embryo sac maturation, while PSK6 showed expression during anther cell differentiation and at pollen maturity, and an expression pattern similar to PSK4 in the female reproductive organs. The results also revealed transcripts of a PSK gene in embryos at the globular stage.

6 3,AB/21 (Item 1 from file: 76)  
DIALOG(R)File 76:Life Sciences Collection  
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02713520 5377769  
The UCU1 **Arabidopsis** Gene Encodes a **SHAGGY/CSK3-like Kinase** Required for Cell Expansion along the Proximodistal Axis  
Perez Perez, J.M.; Ponce, M.R.; Micol, J.L.  
Division de Genetica and Instituto de Biotecnologia, Universidad Miguel Hernandez, Campus de Elche, 03202 Elche, Alicante, Spain  
Developmental Biology vol. 242, no. 2, pp. 161-173 (2002)  
ISSN: 0012-1606  
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH  
SUBFILE: Genetics Abstracts

Most signal transduction pathways central to development are not shared by plants and animals. Such is the case of the Wingless/Wnt signaling pathway, whose components play key roles in metazoan pattern formation and tumorigenesis, but are absent in plants, with the exception of **SHAGGY/CSK3**, a cytoplasmic protein **kinase** represented in the genome of **Arabidopsis thaliana** by a family of 10 AtSK genes for which mutational evidence is scarce. Here, we describe the characterization of mutant alleles of the **Arabidopsis** ULTRACURVATA1 (UCU1) gene, the two strongest of which dramatically reduce cell expansion along the proximodistal axis, dwarfing the mutant plants, whose cells expand properly across but not along most organs. Proximodistal expansion of adaxial (dorsal) and abaxial (ventral) leaf cells exhibits a differential dependence on UCU1 function, as suggested by the leaves of ucul mutants, which are rolled spirally downward in a circinate manner. We have positionally cloned the UCU1 gene, which encodes an AtSK protein involved in the cross-talk between auxin and brassinosteroid signaling pathways, as indicated by the responses of ucul mutants to plant hormones and the phenotypes of double mutants involving ucul alleles.

6 3,AB/22 (Item 2 from file: 76)  
DIALOG(R)File 76:Life Sciences Collection  
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02359959 4495739  
Characterization of three novel members of the **Arabidopsis SHAGGY**-related protein **kinase** (ASK) multigene family  
Dornelas, M.C.; Wittich, P.; von Recklinghausen, I.; van Lammeren, A.; Freis, M.  
Institut de Biotechnologie des Plantes ERS/CNRS 569, Universite de Paris-Sud, Batiment 630, 91405 Orsay Cedex, France  
Plant Molecular Biology vol. 39, no. 1, pp. 137-147 (1999)  
ISSN: 0167-4412  
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH  
SUBFILE: Genetics Abstracts; Biochemistry Abstracts 2: Nucleic Acids

In this paper we report the characterization of three novel members of the **Arabidopsis shaggy**-related protein **kinase** (ASK) multigene family, named ASK<sub>dzeta</sub> (ASK), ASK<sub>eta</sub> (ASK eta) and ASK<sub>iot</sub> (ASK iota). The proteins encoded by the ASK genes share a highly conserved catalytic protein **kinase** domain and show about 70% identity to **SHAGGY** (SGG) and glycogen synthase **kinase-3** (GSK-3) from *Drosophila* and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in *Drosophila*. At least ten different ASK genes are expected to be present per haploid genome of *A. thaliana*. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 sub-family of protein **kinases** demonstrated a clear distinction between the plant and the animal **kinases**. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these **kinases**. The differential expression patterns of five ASK genes were assessed by northern and in situ hybridization experiments using gene-specific probes. While ASK<sub>g</sub>? is expressed in the whole embryo during its development, ASK<sub>eta</sub> expression is limited to the suspensor cells. No signal was detected for ASK alpha, ASK gamma and ASK iota in developing embryos.

6/3,AB/23 (Item 1 from file: 144)  
DIALOG(R)File 144:Pascal  
(c) 2002 INIST/CNRS. All rts. reserv.

15494275 PASCAL No.: 02-0189640  
Regulation of brassinosteroid signaling by a GSK3/**SHAGGY**-like kinase  
JIANMING LI; KYOUNG HEE NAM  
Department of Molecular, Cellular, and Developmental Biology, University of Michigan, Ann Arbor, MI 48109-1048, United States  
Journal: *Science* : (Washington, D.C.), 2002, 295 (5558) 1299-1301  
Language: English  
**GSK3/SHAGGY** is a highly conserved serine/threonine **kinase** implicated in many signaling pathways in eukaryotes. Although many GSK3/**SHAGGY**-like **kinases** have been identified in plants, little is known about their functions in plant growth and development. Here we show that the **Arabidopsis** BRASSINOSTEROID-INSENSITIVE 2 (BIN2) gene encodes a GSK3/**SHAGGY**-like **kinase**. Gain-of-function mutations within its coding sequence or its overexpression inhibit brassinosteroid (BR) signaling, resulting in plants that resemble BR-deficient and BR-response mutants. In contrast, reduced BIN2 expression via cosuppression partially rescues a weak BR-signaling mutation. Thus, BIN2 acts as a negative regulator to control steroid signaling in plants.

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6/3,AB/24 (Item 2 from file: 144)  
DIALOG(R)File 144:Pascal  
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15434165 PASCAL No.: 02-0178662  
Contribution a la caractérisation de la sous-famille des protéines serine/threonine **kinases** du type **SHAGGY/GSK-3** chez **Arabidopsis thaliana**  
(Contribution to the characterization of the **Arabidopsis** thaliana **SHAGGY/GSK-3** subfamily of serine/threonine protein **kinases**)  
TAVARES Raquel; FREIS Martin, dir

Universite de Paris 11, Orsay, France  
Univ.: Universite de Paris 11. Orsay. FRA      Degree: Th. doct.  
2000-12; 2000 232 p.

Language: French   Summary Language: French; English

Chez les animaux, les protéines serine/threonine **kinases** de la famille **SHAGGY** /GSK-3 sont impliquées dans une grande variété de processus biologiques, comme la régulation de l'insuline et la détermination de la destinée et de la prolifération cellulaires. Ce travail de these avait comme objectif de contribuer à l'élucidation des rôles biologiques de ces protéines chez les plantes, plus particulièrement à travers l'identification et l'étude d'un sous-groupe de cette famille chez **Arabidopsis**. L'analyse des séquences des gènes AtSK ( **Arabidopsis thaliana SHAGGY-like Kinases**) du groupe III a permis de compléter les études concernant l'organisation et l'évolution de la famille **shaggy** /GSK-3 chez les plantes. Par ailleurs, la caractérisation de l'environnement génomique des différents paralogues nous a amenés à la caractérisation de la structure et de l'évolution de quatre autres familles multigeniques chez **Arabidopsis**. Des études d'expression des gènes AtSK du groupe III ont été réalisées utilisant des techniques de RT-PCR et de PCR sur des banques d'ADNc. L'immunolocalisation de quatre AtSK a également été effectuée, sur des extraits protéiques et sur des coupes, en utilisant des anticorps spécifiques. La localisation intracellulaire de la protéine AtSK THETA a notamment été déterminée. Enfin, la connaissance des séquences génomiques de la totalité de la famille AtSK nous a permis de tester les fonctions biologiques des différents paralogues par des techniques de génétique inverse. La modification *in vivo* de l'expression des gènes AtSK du groupe III a été entreprise, par le biais de la production de plantes d'**Arabidopsis** comportant des séquences antisens spécifiques. Nous avons utilisé un système de transactivation de l'expression de la séquence antisens dans la descendance de deux lignées, une lignée antisens et une lignée activatrice, présentant un phénotype sauvage.

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6/3,AB/25      (Item 3 from file: 144·  
DIALOG(R)File 144:Pascal  
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15255167      PASCAL No.: 01-0424400  
Constitutive over-expression of AtGSK1 induces NaCl stress responses in the absence of NaCl stress and results in enhanced NaCl tolerance in **Arabidopsis**

HAI LAN PIAO; JEONG HWA LIM; SOO JIN KIM; CHEONG Gang-Won; HWANG Inhwan  
Center for Plant Intracellular Trafficking, Pohang University of Science and Technology, Pohang, 790-784, Korea, Republic of; Department of Biochemistry, Gyeongsang National University, Chinju, 660-701, Korea, Republic of; Division of Molecular and Life Sciences, Pohang University of Science and Technology, Pohang, 790-784, Korea, Republic of

Journal: Plant journal, 2001, 27 (4) 305-314

Language: English

GSK3/**shaggy**-like protein **kinases** have been shown to play diverse roles in development and signal transduction pathways in various organisms. An **Arabidopsis** homologue of GSK3/**shaggy**-like **kinase**, AtGSK1, has been shown to be involved in NaCl stress responses. In order to further clarify the role of AtGSK1 in NaCl stress responses in plants, we generated transgenic **Arabidopsis** plants that over-expressed AtGSK1 mRNA. These plants showed enhanced resistance to NaCl stress when assayed either as whole plants or by measurement of root growth on NaCl plates. In addition, AtGSK1 transgenic plants in the absence of NaCl stress showed phenotypic changes, such as accumulation of anthocyanin, that were similar to those observed in wild-type plants under NaCl stress. Transgenic plants accumulated 30-50% more Na<sup>+</sup> than did wild-type

plants when subjected to NaCl stress, and Ca SUP 2 SUP + content was increased by 15-30% in the transgenic plants regardless of the NaCl stress level. Northern blotting revealed that AtGSK1 over-expression induced expression of the NaCl stress-responsive genes AtCP1, RD29A and CHS1 in the absence of NaCl stress. In addition, AtCBL1 and AtCP1 were super-induced in the NaCl-stressed transgenic plants. Taken together, these results suggest that AtGSK1 is involved in the signal transduction pathway(s) of NaCl stress responses in *Arabidopsis*.

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5.3,AB/26 (Item 4 from file: 144)  
DIALOG(R)File 144:Pascal  
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14249339 PASCAL No.: 99-0452372  
Caracterisation d'homologues de la protéine kinase **SHAGGY**  
chez **Arabidopsis** thaliana et leur rôle biologique pendant le  
développement

(Characterization of *Arabidopsis* thaliana homologues of  
**SHAGGY** protein kinase and their biological role during  
development)

DOPNELAS Marcelo; KREIS Martin, dir  
Université de Paris 11, Orsay, France  
Univ.: Université de Paris 11. Orsay. FFA Degree: Th. doct.  
1999-05; 1999 182 p.

Language: French Summary Language: French; English  
Trois nouveaux membres de la famille multigénique ASK (pour  
**Arabidopsis** **SHAGGY** - related protein **kinases**) nommés  
ASK $\zeta$  (ASK zeta), ASK $\eta$  (ASK eta) et ASK $\iota$  (ASK iota), ont été  
identifiés chez **Arabidopsis** thaliana. Les gènes ASK sont des  
homologues végétaux du gène **SHAGGY** (SGG) chez la *Drosophila*,  
appartenant à la sous-famille GSK-3 des protéines **kinases**. Dans un  
premier temps, la comparaison des séquences d'acides aminés des protéines  
**kinases** de la sous-famille GSK-3 a permis l'identification de trois  
groupes, évolutivement conservés, d'homologues végétaux de SGG. La  
comparaison des séquences nucléotidiques des gènes de la famille ASK a  
permis la proposition d'un modèle d'évolution de cette famille  
multigénique. Par la suite, l'expression des gènes ASK des groupes I et II  
a été étudiée pendant le développement d'**Arabidopsis** utilisant la  
technique d'hybridation *in situ*. Des plantes transgéniques contenant des  
constructions antisens des gènes ASK des groupes I et II ont été obtenues.  
L'analyse des phénotypes des plantes antisens a permis la suggestion d'un  
rôle biologique pour les protéines ASK pendant le développement floral et  
embryonnaire d'**Arabidopsis**.

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5.3,AB/27 (Item 5 from file: 144)  
DIALOG(R)File 144:Pascal  
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14074777 PASCAL No.: 99-0267163  
An **Arabidopsis** GSK3/**shaggy**-like gene that complements yeast  
salt stress-sensitive mutants is induced by NaCl and abscisic acid  
HAI LAN PIAO; KYEONG TAE PIH; JEONG HWA LIM; SHIN GENE KANG; JING BO JIN;  
SUJUNG KIM; HWANG J

Department of Molecular Biology, Gyeongsang National University, Chinju,  
660-701, Korea, Republic of; Plant Molecular Biology and Biotechnology  
Research Center, Gyeongsang National University, Chinju, 660-701, Korea,  
Republic of

Journal: Plant physiology : (Bethesda), 1999, 119 (4) 1527-1534

Language: English

GSK3/**shaggy**-like genes encode **kinases** that are involved in a variety of biological processes. By functional complementation of the yeast calcineurin mutant strain DHT22-1a with a NaCl stress-sensitive phenotype, we isolated the **Arabidopsis** cDNA AtGSK1, which encodes a GSK3/**shaggy**-like protein **kinase**. AtGSK1 rescued the yeast calcineurin mutant cells from the effects of high NaCl. Also, the AtGSK1 gene turned on the transcription of the NaCl stress-inducible PMR2A gene in the calcineurin mutant cells under NaCl stress. To further define the role of AtGSK1 in the yeast cells we introduced a deletion mutation at the MCK1 gene, a yeast homolog of GSK3, and examined the phenotype of the mutant. The mck1 mutant exhibited a NaCl stress-sensitive phenotype that was rescued by AtGSK1. Also, constitutive expression of MCK1 complemented the NaCl-sensitive phenotype of the calcineurin mutants. Therefore, these results suggest that Mck1 p is involved in the NaCl stress signaling in yeast and that AtGSK1 may functionally replace Mck1p in the NaCl stress response in the calcineurin mutant. To investigate the biological function of AtGSK1 in **Arabidopsis** we examined the expression of AtGSK1. Northern blot analysis revealed that the expression is differentially regulated in various tissues with a high level expression in flower tissues. In addition, the AtGSK1 expression was induced by NaCl and exogenously applied ABA but not by KCl. Taken together, these results suggest that AtGSK1 is involved in the osmotic stress response in **Arabidopsis**.

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5/3,AB/28 (Item 6 from file: 144)  
BIBLOG(R)File 144:Pascal  
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11433753 PASCAL No.: 94-0267915

Isolation et caracterisation d'homologues de la proteine **kinase** **shaggy**/GSK-3 chez **Arabidopsis** thaliana et identification d'un gene correspondant chez *Saccharomyces cerevisiae*

(Isolation and characterization of **Arabidopsis** thaliana homologs of the **shaggy**/gsk-3 protein **kinase** and identification of a corresponding gene in *Saccharomyces cerevisiae*)

BIANCHI Michele; KFEIS Martin, dir  
Universite de Paris 11, France  
Univ.: Universite de Paris 11. FRA      Degree: Th. doct.  
1993-09; 1993 155 p.

Language: French   Summary Language: French; English

Les proteines **kinases** (PKs) sont les composants centraux du systeme cybernetique des cellules eucaryotes. L'identification d'homologues de PKs conservees au cours de l'evolution peut constituer une approche complementaire aux techniques genetiques pour l'etude de voies de transduction importantes chez les plantes. Dans un premier temps, une approche de PCR (polymerase chain reaction) a permis d'identifier, chez **Arabidopsis** thaliana, une famille de genes apparentes a (1) MCK1 (meiosis and centromere regulatory **kinase**) de *Saccharomyces cerevisiae*; (2) **shaggy/zeste-white 3**, impliquee dans le developpement de *Drosophila melanogaster*; (3) le gene codant la glycogen synthase **kinase** -3 (GSK-3, regulateur du facteur transcriptionnel c-Jun) de mammiferes. Par la suite, la caracterisation de deux ADNc, ASK-alpha et ASK-gamma (**Arabidopsis shaggy**-related protein **kinase**), a permis de mettre en evidence une identite de 70% au niveau du domaine catalytique, entre les proteines ASK et **shaggy**/GSK-3 dont ils representent donc les homologues vegetaux. L'activite **kinase** ainsi qu'une autophosphorylation sur des residus threonine, serine et, en plus faible quantite, tyrosine, ont pu etre demontrées apres production des proteines ASK dans *E. coli*. Par ailleurs, le niveau relativement faible d'identite avec MCK1 (40%) a mene a la recherche puis a l'isolation d'un

deuxieme gene de *S. cerevisiae*: ScGSK-3, dont le produit putatif est identique a 60%, au niveau du domaine catalytique, avec GSK-3, **shaggy** et les proteines ASK. Une analyse de phylogenie moleculaire a suggere que ScGSK-3 code le veritable homologue de GSK-3 et **shaggy**, alors que MCK1 serait originaire d'un evenement de duplication specifique du lignage de *S. cerevisiae*. L'etude simultanee des PKs de la famille GSK-3 dans differents organismes devrait fournir une aide importante a la comprehension des fonctions biochimiques et biologiques des proteines ASK chez les plantes superieures

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Set	Items	Description
S1	7347	ARABIDOPSIS AND KINAS?
S2	90	S1 AND SHAGGY
S3	55	S1 AND ASK
S4	0	S1 AND DZETA
S5	21	S1 AND ZETA
S6	28	RD S2 (unique items)

: rd a3  
-->'A3' is not a correct set number.  
: rd s3  
-->Duplicate detection is not supported for File 235.  
-->Duplicate detection is not supported for File 306.  
  
-->Records from unsupported files will be retained in the RD set.  
...examined 50 records (50)  
-->Record 266:276026 ignored; incomplete bibliographic data, not retained - in RD set  
...completed examining records  
    S7      22  RD S3 (unique items)  
: s s7 not s6  
    22  S7  
    28  S6  
    S8      15  S7 NOT S6  
: t s8/3,ab/all  
-->No matching display code(s) found in file(s): 65, 235, 306

8/3,AB/1 (Item 1 from file: 155)  
DIALOG(R)File 155: MEDLINE(R)

10579927 20098709 PMID: 10631245  
Identification by large-scale screening of phytochrome-regulated genes in etiolated seedlings of **Arabidopsis** using a fluorescent differential display technique.  
Kuno N; Muramatsu T; Hamazato F; Furuya M  
Hitachi Advanced Research Laboratory, Hatoyama, Saitama 350-0395, Japan.  
Plant physiology (UNITED STATES) Jan 2000, 122 (1) p15-24, ISSN 0032-0889 Journal Code: 0401224  
Document type: Journal Article  
Languages: ENGLISH  
Main Citation Owner: NLM  
Record type: Completed  
Phytochrome A (PhyA)-regulated genes in 6-d-old etiolated seedlings of **Arabidopsis** Landsberg erecta were identified by fluorescent differential display. To screen for PhyA-regulated genes, mRNA fingerprints of the wild type and the phyA-201 mutant were compared from samples prepared 4 h after far-red light irradiation. Approximately 30,000 bands of cDNA were displayed by fluorescent differential display, and 24 differentially expressed bands were observed. Sequence analysis revealed that they represent 20 distinct genes. Among them, 15 genes were confirmed as PhyA regulated by northern-blot (or reverse transcription-polymerase chain reaction) analysis. Thirteen up-regulated genes included 12 known genes that encode nine photosynthetic proteins, two enzymes involved in the biosynthesis of chlorophyll, one DNA damage repair/toleration-related protein, and one unknown gene. Two down-regulated genes were identified as encoding a xyloglucan endotransglycosylase-related protein and a novel member of the ASK protein kinase family. In the phyA-201 mutant and the phyA-201phyB-1 double mutant, expression of all of these genes was photoreversibly up- or down-regulated by type II phytochromes. The results indicate that modes of photoperception differ between PhyA and PhyB, but that both types of phytochromes have overlapping effects on the photoregulation of gene expression.

8/3,AB/2 (Item 1 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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08560820 Genuine Article#: 300TZ Number of References: 51  
Title: **Arabidopsis thaliana** SHAGGY-related protein **kinases**  
(AtSK11 and 12) function in perianth and gynoecium development (ABSTRACT AVAILABLE)  
Author(s): Dornelas MC; vanLammeren AAM; Kreis M (REPRINT)  
Corporate Source: UNIV PARIS 11, INST BIOTECHNOL PLANTES, CNRS, UMR 8618, PATIMENT 630/F-91405 ORSAY//FRANCE// (REPRINT); UNIV PARIS 11, INST BIOTECHNOL PLANTES, CNRS, UMR 8618/F-91405 ORSAY//FRANCE//; AGR UNIV WAGENINGEN, LAB EXPT PLANT MORPHOL & CELL BIOL/NL-6703 BD WAGENINGEN//NETHERLANDS//  
Journal: PLANT JOURNAL, 2000, V21, N5 (MAY), P419-429  
ISSN: 0960-7412 Publication date: 2000-05-01  
Publisher: BLACKWELL SCIENCE LTD, P O BOX 38, OSNEY MEAD, OXFORD OX2 0NE, OXON, ENGLAND  
Language: English Document Type: ARTICLE  
Abstract: In higher plants, the correct patterning of the floral meristem in terms of organ type, number and form is the result of a concerted expression of a network of genes. We describe phenotypes of flower patterning, resulting from a reduction of transcript levels of the **Arabidopsis** SHAGGY-related protein **kinase** genes AtSK11 (ASK alpha) and AtSK12 (ASK gamma). The AtSK genes are plant homologues of the *Drosophila* shaggy (SGG) gene and the mammalian Glycogen-Synthase **Kinase-3** (GSK-3). The SGG protein **kinase** is a key component of the wingless signalling pathway and is required for the establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11 (ASK alpha) and AtSK12 (ASK gamma) genes during wild-type **Arabidopsis** inflorescence development, detected by *in situ* hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11 (ASK alpha) and AtSK12 (ASK gamma) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11 (ASK alpha) and AtSK12 (ASK gamma) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the apical-basal patterning of the gynoecium.

8/3,AB/3 (Item 2 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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06509423 Genuine Article#: YY117 Number of References: 44  
Title: A state-independent interaction between ligand and a conserved arginine residue in cyclic nucleotide-gated channels reveals a functional polarity of the cyclic nucleotide binding site (ABSTRACT AVAILABLE)  
Author(s): Tibbs GR (REPRINT); Liu DT; Leypoldt BG; Sigelbaum SA  
Corporate Source: COLUMBIA UNIV, DEPT PHARMACOL, CTR NEUROBIOL & BEHAV, 722 W 168TH ST, NEW YORK, NY 10032 (REPRINT); COLUMBIA UNIV, HOWARD HUGHES MED INST, NEW YORK, NY 10032  
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N8 (FEB 20), P 4497-4505  
ISSN: 0021-9258 Publication date: 1998-02-20  
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814  
Language: English Document Type: ARTICLE  
Abstract: Activation of cyclic nucleotide-gated channels is thought to

involve two distinct steps: a recognition event in which a ligand binds to the channel and a conformational change that both opens the channel and increases the affinity of the channel for an agonist. Sequence similarity with the cyclic nucleotide binding sites of cAMP- and cGMP-dependent protein **kinases** and the bacterial catabolite activating protein (CAP) suggests that the channel ligand binding site consists of a beta-roll and three alpha-helices. Recent evidence has demonstrated that the third (or C) alpha-helix moves relative to the agonist upon channel activation, forming additional favorable contacts with the purine ring. Here we **ask** if channel activation also involves structural changes in the beta-roll by investigating the contribution of a conserved arginine residue that, in CAP and the **kinases**, forms an important ionic interaction with the cyclized phosphate of the bound ligand. Mutations that conserve, neutralize, or reverse the charge on this arginine decreased the apparent affinity for ligand over four orders of magnitude but had little effect on the ability of bound ligand to open the channel. These data indicate that the cyclized phosphate of the nucleotide approaches to within 2-4 Angstrom of the arginine, forming a favorable ionic bond that is largely unaltered upon activation. Thus, the binding site appears to be polarized into two distinct structural and functional domains: the beta-roll stabilizes the ligand in a state-independent manner, whereas the C-helix selectively stabilizes the ligand in the open state of the channel. It is likely that these distinct contributions of the nucleotide/C-helix and nucleotide/beta-roll interactions may also be a general feature of the mechanism of activation of other cyclic nucleotide-binding proteins.

8/3,AB/4 (Item 3 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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05260701 Genuine Article#: VL534 Number of References: 202  
Title: THE GENES OF PLANT SIGNAL-TRANSDUCTION (Abstract Available)  
Author(s): REDHEAD CR; PALME K  
Corporate Source: MAX PLANCK GESELL,MAX DELBRUCK LAB,CARL VON LINNE WEG  
10 D-50829 COLOGNE/, GERMANY/  
Journal: CRITICAL REVIEWS IN PLANT SCIENCES, 1996, V15, N5-6, P425-454  
ISSN: 0735-2689

Language: ENGLISH Document Type: REVIEW  
Abstract: Due to the enormous importance of plants as a source of both food and raw materials, an understanding of the control of their growth and development is imperative. Basic to this understanding is the identification of the genes that enable the plant to adapt to its environment while at the same time adhering to its basic developmental plan. The aims of this review are first to briefly summarize the various approaches that have been used to identify these plant signaling genes and second to give an overview of the genes that have been cloned so far and what these genes may tell us about the nature of signal transduction in plants. The advent of modern molecular biology and molecular genetics has revolutionized our ability to unravel the complexities of plant signal transduction pathways. A whole battery of techniques are now available to identify the genes that control the plants development and ability to adapt to its environment. (65) Each technique has its own strengths and weaknesses and must be carefully selected by the researcher according to the question that he or she would like to **ask**.

8/3,AB/5 (Item 1 from file: 50)  
DIALOG(R)File 50:CAB Abstracts  
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03433854 CAB Accession Number: 971609343

Differential expression of two functional serine/threonine protein **kinases** from soyabean that have an unusual acidic domain at the carboxy terminus.

Yoon, H. W.; Kim, M. C.; Shin, P. G.; Kim, J. S.; Kim, C. Y.; Lee, S. Y.; Hwang, I.; Bahk, J. D.; Hong, J. C.; Han, C.; Cho, M. J.

Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Chinju 660-701, Korea Republic.

Molecular and General Genetics vol. 255 (4): p.359-371

Publication Year: 1997

ISSN: 0026-8925 --

Language: English

Document Type: Journal article

Two soyabean cDNA clones, SPK3 and SPK4, encoding putative protein **kinases** were isolated and characterized (GenBank accession numbers L19361 and L38855, respectively). Both cDNAs encoded approximately 40 kDa serine/threonine **kinases** with unusual stretches of acidic amino acids in their carboxy-terminal regions, which are highly homologous to the wheat PKABA1 and *Arabidopsis* ASK **kinases**. These **kinases** are encoded by one- or two-copy genes in the soyabean genome. Notably, SPK3 and SPK4 showed different patterns of expression in various soyabean tissues. SPK3 was highly expressed in dividing and elongating tissues of young seedlings, but relatively weakly in tissues of mature plants. In contrast, SPK4 showed relatively high and constitutive expression in all the tissues examined except for leaf tissues of mature plants. Although various stressors, such as dehydration and high salinity, increased the expression of both genes, the induction kinetics were different. The two genes also differed in their response to abscisic acid (ABA). SPK3 was induced but SPK4 was not affected by exogenously supplied abscisic acid. In accordance with these expression data, analysis of the activity of a chimaeric SPK3 promoter:: beta-glucuronidase (GUS) reporter gene by transient expression in tobacco leaves confirmed the inducibility of SPK3 by salt and ABA. Polyclonal antibodies raised against a recombinant SPK4 protein produced in *Escherichia coli* specifically recognized both recombinant SPK3 and SPK4 proteins. **Kinase** assays using affinity-purified SPK4/antibody complexes with crude soyabean extracts as substrate identified specific phosphorylation of two 41 and 170 kDa soyabean proteins that were phosphorylated on serine residues. Taken together, these results suggested that SPK3, and/or SPK4 are functional serine protein **kinase**(s). Furthermore, SPK3 and SPK4 may play different roles in the transduction of various environmental stresses. 47 ref.

8/3,AB/6 (Item 1 from file: 98)  
DIALOG(R:File 98:General Sci Abs/Full-Text  
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04600393 H.W. WILSON RECORD NUMBER: BGSAC16000393  
The ecology and physiology of viviparous and recalcitrant seeds.

Farnsworth, Elizabeth

Annual Review of Ecology and Systematics v. 31 (2000) p. 107-38

SPECIAL FEATURES: bibli graph il tab ISSN: 0066-4162

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 12647

ABSTRACT: Understanding seed physiology is central to reconstructing how angiosperms have evolved, to characterizing dormancy and germination regimes shared by suites of species, and to devising sound strategies for seed bank conservation, agriculture, and forestry. While species with dormant seeds have received the lion's share of attention, hundreds of plant species exhibit no seed dormancy and germinate either viviparously on the parent plant or shortly after release. Embryos of these recalcitrant

and viviparous species cannot tolerate the maturation drying that is usually prerequisite to dormancy; such desiccation intolerance creates challenges for storing and preserving such embryos. I review the physiology, morphology, and ecology of these desiccation-intolerant, nondormant lineages. Differences in the production and function of plant hormones are implicated in the occurrence of recalcitrance and vivipary in plant families. Plant hormones are key regulators of seed physiology and simultaneously coordinate responses of the seedling and mature plant to their environment. Desiccation-intolerant embryos occur most commonly among species of wet or flooded environments and have evolved multiple times in disparate lineages. Natural selection in wetland environments simply may not eliminate these seed types or may select for changes in hormone physiology that simultaneously affect both maternal and embryonic tissues. Integrative data from ecological, genetic, and physiological studies are needed to elucidate evolutionary origins and maintenance of reproductive strategies in organisms. Reprinted by permission of the publisher.

6/3,AB/7 (Item 2 from file: 98)  
SIAMCD(E)File 98:General Sci Abs/Full-Text  
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54362830 H.W. WILSON RECORD NUMBER: BGSA00112830  
Genomic imprinting and environmental disease susceptibility.  
AUGMENTED TITLE: workshop summary  
Sirtle, Randy L  
Sander, Miriam; Barrett, J. Carl  
Environmental Health Perspectives (Environ Health Perspect) v. 108 no.3  
(Mar. 2000) p. 271-8  
SPECIAL FEATURES: bibl ISSN: 0091-6765  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 8761

ABSTRACT: Genomic imprinting is one of the most intriguing subtleties of modern genetics. The term "imprinting" refers to parent-of-origin-dependent gene expression. The presence of imprinted genes can cause cells with a full parental complement of functional autosomal genes to specifically express one allele but not the other, resulting in monallelic expression of the imprinted loci. Genomic imprinting plays a critical role in fetal growth and behavioral development, and it is regulated by DNA methylation and chromatin structure. This paper summarizes the Genomic Imprinting and Environmental Disease Susceptibility Conference held 8-10 October 1998 at Duke University, Durham, North Carolina. The conference focused on the importance of genomic imprinting in determining susceptibility to environmentally induced diseases. Conference topics included rationales for imprinting; parental antagonism and speciation; methods for imprinted gene identification; allelic message display and monochromosomal mouse/human hybrids; properties of the imprinted gene cluster human 11p15.5 and mouse distal 7; the epigenetics of X-chromosome inactivation; variability in imprinting; imprint erasure; non-Mendelian inheritance ratios; and polymorphic imprinting; imprinting and behavior; genetics of bipolar disorder; imprinting in Turner syndrome; and imprinting in brain development and social behavior; and aberrant methylation: methylation and chromatin structure; methylation and estrogen exposure; methylation of tumor suppressor genes; and cancer susceptibility. Environmental factors are capable of causing epigenetic changes in DNA that can potentially alter imprint gene expression and that can result in genetic diseases including cancer and behavioral disorders. Understanding the contribution of imprinting to the regulation of gene expression will be an important step in evaluating environmental influences on human health and disease.  
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8/3,AB/8 (Item 3 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04272504 H.W. WILSON RECORD NUMBER: BGSA00022504  
Swinging arms and swinging domains in multifunctional enzymes: catalytic machines for multistep reactions.  
Perham, Richard N  
Annual Review of Biochemistry v. 69 (2000) p. 961-1004  
SPECIAL FEATURES: bibl il ISSN: 0066-4154  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 19859

ABSTRACT: Multistep chemical reactions are increasingly seen as important in a growing number of complex biotransformations. Covalently attached prosthetic groups or swinging arms, and their associated protein domains, are essential to the mechanisms of active-site coupling and substrate channeling in a number of the multifunctional enzyme systems responsible. The protein domains, for which the posttranslational machinery in the cell is highly specific, are crucially important, contributing to the processes of molecular recognition that define and protect the substrates and the catalytic intermediates. The domains have novel folds and move by virtue of conformationally flexible linker regions that tether them to other components of their respective multienzyme complexes. Structural and mechanistic imperatives are becoming apparent as the assembly pathways and the coupling of multistep reactions catalyzed by these dauntingly complex molecular machines are unraveled. Reprinted by permission of the publisher.

8/3,AB/9 (Item 4 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04269830 H.W. WILSON RECORD NUMBER: BGSA00019830  
Stomatal patterning in angiosperms.  
Crickdale, Judith L  
American Journal of Botany (Am J Bot) v. 87 no8 (Aug. 2000) p. 1069-80  
SPECIAL FEATURES: bibl il ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 11339

ABSTRACT: My thesis is that understanding stomatal patterning requires a holistic perspective. Since stomata are structures critical to the survival of terrestrial plants, they need to be viewed in relation to their function and their interface with other structural components. With this outlook, I begin by discussing pattern types, means of measuring them, advantages of each type of measurement, and then present patterning from evolutionary, physiological, ecological, and organ views. I suggest areas where I believe profitable studies might enable us to better understand stomatal patterning. The final sections of the paper review stomatal patterning on angiosperm leaves and present a theory of patterning. With the abundance of molecular information, and coming genomic sequences and new tools, an opportunity exists to dissect the process of how cells are selected to become different from their neighbors and assume a fate critical to plant survival. Understanding this biological process at the molecular level requires comprehending the broad base on which stomatal patterning rests. Reprinted by permission of the publisher.

8/3,AB/10 (Item 5 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04250935 H.W. WILSON RECORD NUMBER: BGS00000985

Analysis of selection on enzyme polymorphisms.

Eanes, Walter F

Annual Review of Ecology and Systematics v. 30 (1999) p. 301-26

SPECIAL FEATURES: bibl ISSN: 0066-4162

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 12061

ABSTRACT: The role of amino acid polymorphisms in adaptive evolution is considered. Studies of model systems indicate that selection may act on enzyme polymorphisms in metabolic genes. In addition, there is evidence that regulatory changes are superimposed on structural changes. Although metabolic responses to selection are multilocus in nature, all enzymes in contributing pathways may not be equal. Further study is needed to determine the rule for these inequalities.

8/3,AB/11 (Item 6 from file: 98)

DIALOG(R)File 98:General Sci Abs/Full-Text

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04050515 H.W. WILSON RECORD NUMBER: BGS00000985

Circadian programs in cyanobacteria: adaptiveness and mechanism.

AUGMENTED TITLE: review

Johnson, Carl Hirsch

Golden, Susan S

Annual Review of Microbiology v. 53 (1999) p. 389-409

SPECIAL FEATURES: bibl il ISSN: 0066-4227

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 8362

ABSTRACT: At least one group of prokaryotes is known to have circadian regulation of cellular activities--the cyanobacteria. Their "biological clock" orchestrates cellular events to occur in an optimal temporal program, and it can keep track of circadian time even when the cells are dividing more rapidly than once per day. Growth competition experiments demonstrate that the fitness of cyanobacteria is enhanced when the circadian period matches the period of the environmental cycle. Three genes have been identified that specifically affect circadian phenotypes. These genes, *kaiA*, *kaiB*, and *kaic*, are adjacent to each other on the chromosome, thus forming a clock gene cluster. The clock gene products appear to interact with each other and form an autoregulatory feedback loop.

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8/3,AB/12 (Item 7 from file: 98)

DIALOG(R)File 98:General Sci Abs/Full-Text

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04045911 H.W. WILSON RECORD NUMBER: BGS00000985

MCM proteins in DNA replication.

Tye, Bik K

Annual Review of Biochemistry v. 68 (1999) p. 649-86

SPECIAL FEATURES: bibl il ISSN: 0066-4154

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 17809

ABSTRACT: The MCM proteins are essential replication initiation factors originally identified as proteins required for minichromosome maintenance in *Saccharomyces cerevisiae*. The best known among them are a family of six

structurally related proteins, MCM2-7, which are evolutionally conserved in all eukaryotes. The MCM2-7 proteins form a hexameric complex. This complex is a key component of the prereplication complex that assembles at replication origins during early G1 phase. New evidence suggests that the MCM2-7 proteins may be involved not only in the initiation but also in the elongation of DNA replication. Orchestration of the functional interactions between the MCM2-7 proteins and other components of the prereplication complex by cell cycle-dependent protein **kinases** results in initiation of DNA synthesis once every cell cycle. Reprinted by permission of the publisher.

8/3,AB/13 (Item 8 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
(c) 2002 The HW Wilson Co. All rts. reserv.

04014401 H.W. WILSON RECORD NUMBER: BGSI99014401  
Heat-shock proteins, molecular chaperones, and the stress response:  
evolutionary and ecological physiology.  
AUGMENTED TITLE: review  
Feder, Martin E  
Hofmann, Gretchen E  
Annual Review of Physiology (Annu Rev Physiol) v. 61 ('99) p. 243-82  
SPECIAL FEATURES: bibl il ISSN: 0066-4278  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 20648

ABSTRACT: Molecular chaperones, including the heat-shock proteins (Hsps), are a ubiquitous feature of cells in which these proteins cope with stress-induced denaturation of other proteins. Hsps have received the most attention in model organisms undergoing experimental stress in the laboratory, and the function of Hsps at the molecular and cellular level is becoming well understood in this context. A complementary focus is now emerging on the Hsps of both model and nonmodel organisms undergoing stress in nature, on the roles of Hsps in the stress physiology of whole multicellular eukaryotes and the tissues and organs they comprise, and on the ecological and evolutionary correlates of variation in Hsps and the genes that encode them. This focus discloses that (a) expression of Hsps can occur in nature, (b) all species have hsp genes but they vary in the patterns of their expression, (c) Hsp expression can be correlated with resistance to stress, and (d) species' thresholds for Hsp expression are correlated with levels of stress that they naturally undergo. These conclusions are now well established and may require little additional confirmation; many significant questions remain unanswered concerning both the mechanisms of Hsp-mediated stress tolerance at the organismal level and the evolutionary mechanisms that have diversified the hsp genes. With permission, from the Annual Review of Physiology, Volume 61, 1999, by Annual Reviews Inc. (<http://www.annurev.org> ).

8/3,AB/14 (Item 9 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
(c) 2002 The HW Wilson Co. All rts. reserv.

03506131 H.W. WILSON RECORD NUMBER: BGSI97006131  
Genetic and molecular analysis of circadian rhythms.  
Dunlap, Jay C  
Annual Review of Genetics (Annu Rev Genet) v. 30 ('96) p. 579-601  
SPECIAL FEATURES: bibl il ISSN: 0066-4197  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 11723

ABSTRACT: The genetic and molecular bases of circadian rhythms are reviewed. Most of the current evidence suggests that biological clocks are based on negative feedback loops involving the rhythmic expression of proteins that shut off their own synthesis. The 2 best understood circadian systems are those of *Neurospora* (frequency (frq) gene) and *Drosophila* (period (per) and timeless genes). Most organisms appear to use a day-phased oscillator similar to that of *Neurospora* rather than the night-phased system of *Drosophila*. Both frq and per are widely conserved within their corresponding phylogenetic classes. Studies of the molecular basis of biological clocks have focused on 3 main areas: the underlying biochemical and genetic bases of oscillators, the synchronization of the oscillator with the geophysical cycles of the external world, and the means by which the clock alters the behavior of the cell and the organism.

8.3,AB/15 (Item 1 from file: 357)  
DIALOG(R)File 357:Derwent Biotech Res.  
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0230234 DBA Accession No.: 99-00335  
APS-**kinase** from **Arabidopsis** thaliana: genomic organization, expression, and kinetic analysis of the recombinant enzyme - recombinant adenylylsulfate-**kinase** expression and characterization  
AUTHOR: Lee S; +Leustek T  
CORPORATE AFFILIATE: Univ.New-Jersey-State  
CORPORATE SOURCE: Biotech Center and Plant Science Department, Rutgers University, 59 Dudley Road, New Brunswick, NJ 08901-8250, USA.  
email:leustek@aesop.rutgers.edu

JOURNAL: Biochem.Biophys.Res.Commun. (247, 1, 171-75) 1998  
ISSN: 0006-291X CODEN: BBRCA9

LANGUAGE: English

ABSTRACT: To determine whether adenylylsulfate-**kinase** (ASK, EC-2.7.1.25) in plants differs kinetically from that in *Escherichia coli* and *Penicillium chrysogenum*, a cDNA encoding ASK was cloned from **Arabidopsis** thaliana by functional complementation of a met14 mutant strain of *Saccharomyces cerevisiae*. ASK could also complement an *Escherichia coli* cysC strain. ASK was expressed as a recombinant protein by cloning the cDNA as a 980 bp BgIII-BamHIH fragment into plasmid pGEX-2T and separately into plasmid pMAL-c2, followed by transformation of *E. coli* JM81A. The properties of recombinant ASK are described. The gene encoding ASK was shown to be composed of 7 exons, interrupted by 6 introns. Recombinant ASK was able to enter isolated intact chloroplasts and showed maximum activity at 10 uM substrate with 5 mM ATP, but was inhibited by more than 10 uM adenylylsulfate. The enzyme had a Vmax of 1.2 umol/min.mg at 25 deg and pH 8, and a Km value of 3.6 uM adenylylsulfate and 1.8 mM ATP. (25 ref)

?

Set Items Description  
S1 7347 ARABIDOPSIS AND KINAS?  
S2 90 S1 AND SHAGGY  
S3 55 S1 AND ASK  
S4 6 S1 AND DZETA  
S5 21 S1 AND ZETA  
S6 28 RD S2 (unique items)  
S7 22 RD S3 (unique items)  
S8 15 S7 NOT S6

? rd s5

>>>Duplicate detection is not supported for File 235.  
>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.  
...completed examining records

S9 19 RD S5 (unique items)  
? s s9 not (s6 or s7)  
19 S9  
28 S6  
22 S7

S10 18 S9 NOT (S6 OR S7)

? t s10/3,ab/all  
>>>No matching display code(s) found in file(s): 65, 235, 306

10/3,AB/1 (Item 1 from file: 155)  
DIALOG(R) File 155: MEDLINE(R)

12679520 21553151 PMID: 11696349  
Differential subcellular localization of hZip1 in adherent and non-adherent cells.

Milon B; Dhermy D; Pountney D; Bourgeois M; Beaumont C  
INSERM U409 and IFR Claude Bernard, Faculte Xavier Bichat, P.O. Box 416,  
16 Rue Henri Huchard, 75018 Cedex 18, Paris, France.  
FEBS letters (Netherlands) Nov 2 2001, 507 (3) p241-6, ISSN

0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Two human divalent cation transporters of the ZIP family, hZip1 and hZip2, homologous to Irt1 (*Arabidopsis thaliana*), the first identified member, have been described. They were shown by transfection into K562 cells to be localized at the plasma membrane and to mediate zinc uptake. Here we report a differential subcellular localization of hZip1 according to cell type. By transient expressions of EGFP-hZip1, FLAG-tagged or native hZip1, we observed that hZip1 has a vesicular localization in COS-7 cells or in several epithelial cell lines, corresponding partially to the endoplasmic reticulum. Using anti-hZip1 antibodies, we confirmed the intracellular localization of the endogenous protein in PC-3, a prostate cancer cell line.

10/3,AB/2 (Item 2 from file: 155)  
DIALOG(R) File 155: MEDLINE(R)

11259916 21287186 PMID: 11389759

*Arabidopsis* IRT2 gene encodes a root-periphery iron transporter.  
Vert G; Briat J F; Curie C

Laboratoire de Biochimie et Physiologie Moleculaire des Plantes, UMR 5004  
CNRS/INRA/Agro-M/Universite Montpellier II, 2 place Viala, F 34060  
Montpellier CEDEX 1, France.

Plant journal : for cell and molecular biology (England) Apr 2001, 26  
(2) p181-9, ISSN 0960-7412 Journal Code: 9207397

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Iron uptake from the soil is a tightly controlled process in plant roots, involving specialized transporters. One such transporter, IRT1, was identified in *Arabidopsis thaliana* and shown to function as a broad-range metal ion transporter in yeast. Here we report the cloning and characterization of the IRT2 cDNA, a member of the ZIP family of metal transporters, highly similar to IRT1 at the amino-acid level. IRT2 expression in yeast suppresses the growth defect of iron and zinc transport yeast mutants and enhances iron uptake and accumulation. However, unlike IRT1, IRT2 does not transport manganese or cadmium in yeast. IRT2 expression is detected only in roots of *A. thaliana* plants, and is upregulated by iron deficiency. By fusing the IRT2 promoter to the uidA reporter gene, we show that the IRT2 promoter is mainly active in the external cell layers of the root subapical zone, and therefore provide the first tissue localization of a plant metal transporter. Altogether, these data support a role for the IRT2 transporter in iron and zinc uptake from the soil in response to iron-limited conditions.

10 3,AB/3 (Item 3 from file: 155)

DIALOG(R)File 155: MEDLINE(R)

11237837 21249805 PMID: 11352462

Two iron-regulated cation transporters from tomato complement metal uptake-deficient yeast mutants.

Eckhardt U; Mas Marques A; Buckhout T J

Humboldt-Universität zu Berlin, Institut für Biologie, Angewandte Botanik, Germany. [ulrich.eckhardt@rz.hu-berlin.de](mailto:ulrich.eckhardt@rz.hu-berlin.de)

Plant molecular biology (Netherlands) Mar 2001, 45 (4) p437-48, ISSN 0167-4412 Journal Code: 9106343

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Although iron deficiency poses severe nutritional problems to crop plants, to date iron transporters have only been characterized from the model plant *Arabidopsis thaliana*. To extend our molecular knowledge of Fe transport in crop plants, we have isolated two cDNAs (LeIRT1 and LeIRT2) from a library constructed from roots of iron-deficient tomato (*Lycopersicon esculentum*) plants, using the *Arabidopsis* iron transporter cDNA, IRT1, as a probe. Their deduced polypeptides display 64% and 62% identical amino acid residues to the IRT1 protein, respectively. Transcript level analyses revealed that both genes were predominantly expressed in roots. Transcription of LeIRT2 was unaffected by the iron status of the plant, while expression of LeIRT1 was strongly enhanced by iron limitation. The growth defect of an iron uptake-deficient yeast (*Saccharomyces cerevisiae*) mutant was complemented by LeIRT1 and LeIRT2 when ligated to a yeast expression plasmid. Transpcrt assays revealed that iron uptake was restored in the transformed yeast cells. This uptake was temperature-dependent and saturable, and Fe<sup>2+</sup> rather than Fe<sup>3+</sup> was the preferred substrate. A number of divalent metal ions inhibited Fe<sup>2+</sup> uptake when supplied at 100-fold or 10-fold excess. Manganese, zinc and copper uptake-deficient yeast mutants were also rescued by the two tomato cDNAs, suggesting that their gene products have a broad substrate range. The gene structure was determined by polymerase chain reaction experiments and, surprisingly, both genes are arranged in tandem with a tail-to-tail orientation.

10/3,AB/4 (Item 1 from file: 10)

DIALOG(R)File 10: AGRICOLA

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3624570 20605899 Holding Library: AGL

Opioid peptide gene expression in the primary hereditary cardiomyopathy of the Syrian hamster. III. Autocrine stimulation of prodynorphin gene expression by dynorphin B

Ventura, C. Pintus, G.

University of Sassari, Sassari, Italy.

Bethesda, Md. : American Society for Biochemistry and Molecular Biology. The Journal of biological chemistry. Mar 7, 1997. v. 272 (10) p. 6799-6804.

ISSN: 0021-9258 CODEN: JBCHA3

ENAL CALL NO: 381 J824

Language: English

Prodynorphin mRNA and dynorphin B expression have been previously shown to be greatly increased in cardiac myocytes of B10 14.6 cardiomyopathic hamsters. Here we report that exogenous dynorphin B induced a dose-dependent increase in prodynorphin mRNA levels and stimulated prodynorphin gene transcription in normal hamster myocytes. Similar responses were elicited by the synthetic selective opioid receptor agonist U-50,488H. These effects were counteracted by the kappa opioid receptor antagonist Mr-1452 and were not observed in the presence of chelerythrine or calphostin C, two specific protein kinase C (PKC) inhibitors. Treatment of cardiomyopathic cells with Mr-1452 significantly decreased both prodynorphin mRNA levels and prodynorphin gene transcription. In control myocytes, dynorphin B induced the translocation of PKC-alpha to the nucleus and increased nuclear PKC activity without affecting the expression of PKC-delta, epsilon, or -zeta. Acute release of either U-50,488H or dyn B over single normal or cardiomyopathic cells transiently increased the cytosolic Ca<sup>2+</sup> concentration. A sustained treatment with each opioid agonist increased the cytosolic Ca<sup>2+</sup> level for a more prolonged period in cardiomyopathic than in control myocytes and led to a depletion of Ca<sup>2+</sup> from the sarcoplasmic reticulum in both groups of cells. The possibility that prodynorphin gene expression may affect the function of the cardiomyopathic cell through an autocrine mechanism is discussed.

10/3,AE/5 (Item 1 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

10586196 Genuine Article#: 544D0 Number of References: 42

Title: The **Arabidopsis** phospholipase D family. Characterization of a calcium-independent and phosphatidylcholine-selective PLD **zeta** 1 with distinct regulatory domains (ABSTRACT AVAILABLE)

Author(s): Qin CB; Wang XM (REPRINT)

Corporate Source: Kansas State Univ,Dept Biochem,Manhattan/KS/66506 (REPRINT); Kansas State Univ,Dept Biochem,Manhattan/KS/66506

Journal: PLANT PHYSIOLOGY, 2002, V128, N3 (MAR), P1057-1068

ISSN: 0032-0889 Publication date: 20020300

Publisher: AMER SOC PLANT BIOLOGISTS, 16501 MONONA DRIVE, ROCKVILLE, MD 20856 USA

Language: English Document Type: ARTICLE

Abstract: Four types of phospholipase D (PLD), PLDalpha, beta, gamma, and delta, have been characterized in **Arabidopsis**, and they display different requirements for Ca<sup>2+</sup>, phosphatidylinositol 4,5-bisphosphate (PIP<sub>2</sub>), substrate vesicle composition, and/or free fatty acids. However, all previously cloned plant PLDs contain a Ca<sup>2+</sup>-dependent phospholipid-binding C2 domain and require Ca<sup>2+</sup> for activity. This study documents a new type of PLD, PLDzeta1, which is distinctively different from previously characterized PLDs. It contains at the N terminus a Phox homology domain and a pleckstrin homology domain, but not the C2 domain. A full-length cDNA for **Arabidopsis** PLDzeta1 has been identified and used to express catalytically active PLD in

Escherichia coli. PLDzeta1 does not require Ca2+ or any other divalent cation for activity. In addition, it selectively hydrolyzes phosphatidylcholine, whereas the other **Arabidopsis** PLDs use several phospholipids as substrates. PLDzeta1 requires PIP2 for activity, but unlike the PIP2-requiring PLDbeta or gamma, phosphatidylethanolamine is not needed in substrate vesicles. These differences are described, together with a genomic analysis of 12 putative **Arabidopsis** PLD genes that are grouped into alpha, beta, delta, gamma, and **zeta** based on their gene architectures, sequence similarities, domain structures, and biochemical properties.

10/3,AB/6 (Item 2 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

07958476 Genuine Article#: 229KH Number of References: 40  
Title: Nuclear localization of protein kinase U-alpha is regulated by 14-3-3 (ABSTRACT AVAILABLE)  
Author(s): Zhang SS; Xing HM; Muslin AJ (REPRINT)  
Corporate Source: WASHINGTON UNIV,SCH MED, CARDIOVASC RES CTR, DEPT MED, BOX 6086, 660 S EUCLID AVE/ST LOUIS//MO/63110 (REPRINT); WASHINGTON UNIV,SCH MED, CARDIOVASC RES CTR, DEPT MED/ST LOUIS//MO/63110; WASHINGTON UNIV,SCH MED, CARDIOVASC RES CTR, DEPT CELL BIOL & PHYSIOL/ST LOUIS//MO/63110  
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1999, V274, N35 (AUG 27), P 24865-24872  
ISSN: 0021-9258 Publication date: 19990827  
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814  
Language: English Document Type: ARTICLE  
Abstract: 14-3-3 proteins are intracellular, dimeric molecules that bind to and modify the activity of several signaling proteins. We used human 14-3-3 **zeta** as a bait in the yeast two-hybrid system to screen a murine embryonic cDNA library. One interacting clone was found to encode the carboxyl terminus of a putative protein kinase. The coding sequence of the human form (protein kinase U alpha, PKU alpha) of this protein kinase was found in GenBank(TM) on the basis of sequence homology. The two-hybrid clone was also highly homologous to TOUSLED, an **Arabidopsis** thaliana protein kinase that is required for normal flower and leaf development. PKU alpha has been found by coimmunoprecipitation to bind to 14-3-3 **zeta** in vivo. Our confocal laser immunofluorescence microscopic experiments revealed that PKU alpha colocalizes with the cytoplasmic intermediate filament system of cultured fibroblasts in the G(1) phase of the cell cycle. PKU alpha is found in the perinuclear area of S phase cells and in the nucleus of late G(2) cells. Transfection of cells with a dominant negative form of 14-3-3 eta promotes the nuclear localization of PKU alpha. These results suggest that the subcellular localization of PKU alpha is regulated, at least in part, by its association with 14-3-3.

10/3,AB/7 (Item 3 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

07814896 Genuine Article#: 201NY Number of References: 58  
Title: Plant MAP kinase kinase kinases structure, classification and evolution (ABSTRACT AVAILABLE)  
Author(s): Jouannic S; Hamal A; Leprince AS; Tregear JW; Kreis M; Henry Y (REPRINT)  
Corporate Source: UNIV PARIS 11,INST BIOTECHNOL PLANTES, LAB BIOL DEV PLANTES, UMR 6818, BATIMENT 630 F-91405 ORSAY, FRANCE/ (REPRINT); UNIV

PARIS 11, INST BIOTECHNOL PLANTES, LAB BIOL DEV PLANTES, UMR 6818/F-91405 ORSAY//FRANCE/  
Journal: GENE, 1999, V233, N1-2 (JUN 11), P1-11  
ISSN: 0378-1119 Publication date: 19990611  
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS  
Language: English Document Type: REVIEW  
Abstract: The increasing number of reports describing plant MAP kinase signalling components reflects the cardinal role that MAP kinase pathways are likely to play during plant growth and development. Relationship and structural analyses of plant MAP kinase kinase kinase related cDNAs and genes established, on one hand, the PMEKKs, which may be distinguished into the alpha, beta, gamma, and **zeta** groups, and, on the other hand, the PRAFs that consist of the delta, eta and theta groups. Plant MAP3Ks are characterized by different primary structures, but conserved within a single group. A relationship analysis, which included animal, fungal and plant MAP3Ks, revealed a high degree of diversity among this biochemically established set of proteins, thus suggesting a range of biological functions. Four major families emerged, namely the MEKK/STE11, including the PMEKKs, the RAF, including the PRAFs, as well as the MLK and CDC7 families. These four families showed phylum-dependent distributions. Signature sequences characterizing the RAF family and the RAF subfamilies have been evidenced. However, no equivalent sequence motifs were identified for the MEKK/STE11 family, which is highly heterogeneous. (C) 1999 Elsevier Science B.V. All rights reserved.

10/3,AB/8 (Item 4 from file: 34)  
DIALOG(R:File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

07489949 Genuine Article#: 172TE Number of References: 53  
Title: Characterization of three novel members of the **Arabidopsis** SHAGGY-related protein **kinase** (ASK) multigene family (ABSTRACT AVAILABLE:  
Author(s): Dornelas MC; Wittich P; vonRecklinghausen I; vanLammeren A; Kreis M (REPRINT)  
Corporate Source: UNIV PARIS 11, INST BIOTECHNOL PLANTES, ERS CNRS 569, BATIMENT 630/F-91405 ORSAY//FRANCE/ (REPRINT); UNIV PARIS 11, INST BIOTECHNOL PLANTES, ERS CNRS 569/F-91405 ORSAY//FRANCE/; AGR UNIV WAGENINGEN, LAB PLANT CYTOL & MORPHOL/NL-6703 BD WAGENINGEN//NETHERLANDS/  
Journal: PLANT MOLECULAR BIOLOGY, 1999, V39, N1 (JAN), P137-147  
ISSN: 0167-4412 Publication date: 19990100  
Publisher: KLUWER ACADEMIC PUBL, SPUIBOULEVARD 50, PO BOX 17, 3300 AA DORDRECHT, NETHERLANDS  
Language: English Document Type: ARTICLE  
Abstract: In this paper we report the characterization of three novel members of the **Arabidopsis** shaggy-related protein **kinase** (ASK) multigene family, named ASKdzeta (ASK **zeta**), ASKetha (ASK eta) and ASK iota (ASK iota). The proteins encoded by the ASK genes share a highly conserved catalytic protein **kinase** domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase **kinase**-3 (GSK-3) from *Drosophila* and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in *Drosophila*. At least ten different ASK genes are expected to be present per haploid genome of *A. thaliana*. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein **kinases** demonstrated a clear distinction

between the plant and the animal **kinases**. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these **kinases**. The differential expression patterns of five ASK genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While ASK **zeta** is expressed in the whole embryo during its development, ASK eta expression is limited to the suspensor cells. No signal was detected for ASK alpha, ASK gamma and ASK iota in developing embryos.

10/3,AB/9 (Item 5 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

06260890 Genuine Article#: YE942 Number of References: 24  
Title: Subunit composition of pre-T cell receptor complexes expressed by primary thymocytes: CD3 delta is physically associated but not functionally required (ABSTRACT AVAILABLE)  
Author(s): Berger MA (REPRINT) ; Dave V; Rhodes MF; Bosma GC; Bosma MJ; Kappes DJ; Wiest DL  
Corporate Source: FOX CHASE CANC CTR, DIV BASIC SCI, IMMUNOBIOLOGY WORKING GRP, 7701 BUPHOLME AVE/PHILADELPHIA//PA/19111 (REPRINT)  
Journal: JOURNAL OF EXPERIMENTAL MEDICINE, 1997, V186, N9 (NOV 3), P 1461-1467  
ISSN: 0022-1107 Publication date: 19971103  
Publisher: ROCKEFELLER UNIV PRESS, 1114 FIRST AVE, 4TH FL, NEW YORK, NY 10021  
Language: English Document Type: ARTICLE  
Abstract: Maturation of immature CD4(-)CD8(-) (DN) thymocytes to the CD4(+)CD8(+) (DP) stage of development is driven by signals transduced through a pre-T cell receptor (TCR) complex, whose hallmark is a novel subunit termed pre-T alpha (pT alpha). However, the precise role of pre-TCRs in mediating the DN to DP transition remains unclear. Moreover, progress in understanding pre-TCR function has been hampered thus far because previous attempts to demonstrate expression of pT alpha-containing pre-TCRs on the surface of normal thymocytes have been unsuccessful. In this report, we demonstrate for the first time that pT alpha-containing pre-TCR complexes are expressed at low levels on the surface of primary thymocytes and that these pre-TCR complexes comprise a disulfide-linked pT alpha-TCR-beta heterodimer associated not only with CD3-gamma and -epsilon, as previously reported, but also with **zeta** and delta. Interestingly, while CD3-delta is associated with the pre-TCR complex, it is not required for pre-TCR function, evidenced by the generation of normal numbers of DP thymocytes in CD3-delta-deficient mice. The fact that any of the signaling components of the pre-TCR are dispensable for pre-TCR function is indeed surprising, given that few pre-TCR complexes are actually expressed on the surface of primary thymocytes *in vivo*. Thus, pre-TCRs do not require the full array of TCR-associated signaling subunits (gamma, delta, epsilon, and **zeta**), possibly because pT alpha itself possesses signaling capabilities.

10/3,AB/10 (Item 6 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

06205693 Genuine Article#: YE663 Number of References: 43  
Title: 14-3-3 inhibits the Dictyostelium myosin II heavy-chain-specific protein **kinase C** activity by a direct interaction: Identification of the 14-3-3 binding domain (ABSTRACT AVAILABLE)  
Author(s): MattoVelin M; Aitken A; Ravid S (REPRINT)

Corporate Source: HEBREW UNIV JERUSALEM, HADASSAH MED SCH, DEPT BIOCHEM/IL-91120 JERUSALEM//ISRAEL/ (REPRINT); HEBREW UNIV JERUSALEM, HADASSAH MED SCH, DEPT BIOCHEM/IL-91120 JERUSALEM//ISRAEL/; NATL INST MED RES, LAB PROT STRUCT/LONDON NW7 1AA//ENGLAND/

Journal: MOLECULAR BIOLOGY OF THE CELL, 1997, V8, N10 (OCT), P1889-1899

ISSN: 1059-1524 Publication date: 19971000

Publisher: AMER SOC CELL BIOLOGY, PUBL OFFICE, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE

Abstract: Myosin II heavy chain (MHC) specific protein **kinase C** (MHC-PKC), isolated from *Dictyostelium discoideum*, regulates myosin II assembly and localization in response to the chemoattractant cyclic AMP. Immunoprecipitation of MHC-PKC revealed that it resides as a complex with several proteins. We show herein that one of these proteins is a homologue of the 14-3-3 protein (Dd14-3-3). This protein has recently been implicated in the regulation of intracellular signaling pathways via its interaction with several signaling proteins, such as PKC and Raf-1 **kinase**. We demonstrate that the mammalian 14-3-3 **zeta** isoform inhibits the MHC-PKC activity in vitro and that this inhibition is carried out by a direct interaction between the two proteins. Furthermore, we found that the cytosolic MHC-PKC, which is inactive, formed a complex with Dd14-3-3 in the cytosol in a cyclic AMP-dependent manner, whereas the membrane-bound active MHC-PKC was not found in a complex with Dd14-3-3. This suggests that Dd14-3-3 inhibits the MHC-PKC in vivo. We further show that MHC-PKC binds Dd14-3-3 as well as 14-3-3 **zeta** through its C1 domain, and the interaction between these two proteins does not involve a peptide containing phosphoserine as was found for Raf-1 **kinase**. Our experiments thus show an in vivo function for a member of the 14-3-3 family and demonstrate that MHC-PKC interacts directly with Dd14-3-3 and 14-3-3 **zeta** through its C1 domain both in vitro and in vivo, resulting in the inhibition of the **kinase**.

10/3, AB/11 (Item 7 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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05955525 Genuine Article#: XK147 Number of References: 65  
Title: An amphibian CD3 homologue of the mammalian CD3 gamma and delta genes (ABSTRACT AVAILABLE)

Author(s): Dzialo RC; Cooper MD (REPRINT)

Corporate Source: UNIV ALABAMA, WALLACE INST 378, DEPT MED, DIV DEV & CLIN IMMUNOL/BIRMINGHAM//AL/35294 (REPRINT); UNIV ALABAMA, WALLACE INST 378, DEPT MED, DIV DEV & CLIN IMMUNOL/BIRMINGHAM//AL/35294; UNIV ALABAMA, DEPT PEDIAT, DIV DEV & CLIN IMMUNOL/BIRMINGHAM//AL/35294; UNIV ALABAMA, DEPT MICROBIOL, DIV DEV & CLIN IMMUNOL/BIRMINGHAM//AL/35294; HOWARD HUGHES MED INST//BIRMINGHAM, AL 35294

Journal: EUROPEAN JOURNAL OF IMMUNOLOGY, 1997, V27, N7 (JUL), P1640-1647

ISSN: 0014-2980 Publication date: 19970700

Publisher: VCH PUBLISHERS INC, 303 NW 12TH AVE, DEERFIELD BEACH, FL 33442-1788

Language: English Document Type: ARTICLE

Abstract: T cell receptor (TCR) genes have been identified in representatives of both cartilaginous and bony vertebrates. The CD3 chains that serve as signal transducing elements of the TCR complex in mammals have been defined to a limited extent in birds. In these studies a CD3 homologue was identified in an amphibian representative, *Xenopus laevis*, using degenerate oligomer primers designed from conserved regions of avian and mammalian CD3 gamma/delta subunits. The reverse transcriptase polymerase chain reaction amplified product of *Xenopus* splenocyte RNA was then used to isolate full-length cDNA clones from a splenic library. When employed as probes, the cDNA clones hybridized with a 1-kb mRNA transcript in *Xenopus* T cells, but not in

other cell types. Comparison of the deduced amino acid sequence indicated a similar degree of homology with mammalian and avian CD3 gamma and delta chains. Genomic analysis indicated that the Xenopus CD3 molecule is encoded by five exons, a structure resembling the mammalian CD3 delta gene rather than the seven exon CD3 gamma gene. Southern blot analysis and sequencing of the 5' flanking region failed to yield evidence of a related Xenopus gene. This amphibian CD3 gene thus appears to represent an ancestral form of the mammalian CD3 gamma and delta genes.

10/3,AB/12 (Item 8 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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05916662 Genuine Article#: XG579 Number of References: 45  
Title: A spontaneously arising mutation in the DLAARN motif of murine ZAP-70 abrogates **kinase** activity and arrests thymocyte development (ABSTRACT AVAILABLE)  
Author(s): Wiest DL; Ashe JM; Howcroft TK; Lee HM; Kemper DM; Negishi I; Singer DS; Singer A (REPRINT) ; Abe R  
Corporate Source: FOX CHASE CANC CTR, DIV BASIC SCI/PHILADELPHIA//PA/19111 (REPRINT); NCI, EXPT IMMUNOL BRANCH, NIH/BETHESDA//MD/20892; USN, MED RES INST, IMMUNE CELL BIOL DEPT/BETHESDA//MD/20889; NIPPON ROCHE RES CTR, KAMAKURA/KANAGAWA 247/JAPAN/; SCI UNIV TOKYO, RES INST BIOL SCI, DIV IMMUNOBIOCL/TOKYO/CHIBA 278/JAPAN/  
Journal: IMMUNITY, 1997, V6, N6 (JUN), P663-671  
ISSN: 1074-7613 Publication date: 19970600  
Publisher: CELL PRESS, 1050 MASSACHUSETTES AVE, CIRCULATION DEPT, CAMBRIDGE, MA 02138  
Language: English Document Type: ARTICLE  
Abstract: Development of immature CD4(+)CD8(+) thymocytes into functionally mature CD4(+) and CD8(+) T cells is driven by selection events that require signals transduced through the T cell antigen receptor (TCR). Transduction of TCR signals in the thymus involves tyrosine phosphorylation of the protein tyrosine **kinase** ZAP-70 by p56(lck) and results in induction of ZAP-70 enzymatic activity. We have identified a novel, spontaneously arising point mutation within a highly conserved motif (DLAARN) in the **kinase** domain of murine ZAP-70 that uncouples tyrosine phosphorylation of ZAP-70 from induction of ZAP-70 **kinase** activity. Mice homozygous for this mutation are devoid of mature T cells because thymocyte development is arrested at the CD4(+)CD8(+) stage of differentiation. The developmental arrest is due to the inability of CD4(+)CD8(+) thymocytes to propagate TCR signals in the absence of ZAP-70 **kinase** activity despite tyrosine phosphorylation of TCR-associated ZAP-70 molecules.

10/3,AB/13 (Item 9 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

05881644 Genuine Article#: XE034 Number of References: 54  
Title: Subcellular localization and ubiquitin-conjugating enzyme (E2) interactions of mammalian HECT family ubiquitin protein ligases (ABSTRACT AVAILABLE)  
Author(s): Hatakeyama S; Jensen JP; Weissman AM (REPRINT)  
Corporate Source: NCI, LAB IMMUNE CELL BIOL, DIV BASIC SCI, NIH, BLDG 10, RM 1B34, 9000 ROCKVILLE BETHESDA//MD/20892 (REPRINT); NCI, LAB IMMUNE CELL BIOL, DIV BASIC SCI, NIH/BETHESDA//ME/20892  
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1997, V272, N24 (JUN 13), P 15085-15092  
ISSN: 0021-9258 Publication date: 19970613  
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE

PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE

Abstract: In most instances, the transfer of ubiquitin to target proteins is catalyzed by the action of ubiquitin protein ligases (E3s). Full-length cDNAs encoding murine E6-associated protein (mE6-AP) as well as Nedd-4, a protein that is homologous to E6-AP in its C terminus, were cloned. Nedd-4 and mouse E6-AP are both enzymatically active E3s and function with members of the UbcH5 family of E2s. Mouse E6-AP, like its human counterpart, ubiquitinates p53 in the presence of human papilloma virus E6 protein, while Nedd-4 does not. Consistent with its role in p53 ubiquitination, mE6-AP was found both in the nucleus and cytosol, while Nedd-4 was found only in the cytosol. Binding studies implicate a 150-amino acid region that is 40% identical between mE6-AP and Nedd-4 as a binding site for the C terminal portion of an E2 enzyme (UbcH5B). Nedd-4 was determined to have a second nonoverlapping E2 binding site that recognizes the first 67 amino acids of UbcH5B but not the more C-terminal portion of this E2. These findings provide the first demonstration of physical interactions between mammalian E2s and E3s and establish that these interactions occur independently of ubiquitin and an intact E3 catalytic domain. Furthermore, the presence of two E2 binding sites within Nedd-4 suggests models for ubiquitination involving multiple E2 enzymes associated with E3s.

10/3,AB/14 Item 10 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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05821731 Genuine Article#: XA029 Number of References: 60  
Title: 14-3-3 epsilon positively regulates Ras-mediated signaling in *Drosophila* (ABSTRACT AVAILABLE)  
Author(s): Chang HC; Rubin GM (REPRINT)  
Corporate Source: UNIV CALIF BERKELEY, HOWARD HUGHES MED INST, DEPT CELL & MOL BIOL/BERKELEY//CA/94720 (REPRINT); UNIV CALIF BERKELEY, HOWARD HUGHES MED INST, DEPT CELL & MOL BIOL/BERKELEY//CA/94720  
Journal: GENES & DEVELOPMENT, 1997, V11, N9 (MAY 1), P1132-1139  
ISSN: 0890-9369 Publication date: 1997/5/1  
Publisher: COLD SPRING HARBOR LAB PRESS, 1 BUNGLOW RD, PLAINVIEW, NY 11724  
Language: English Document Type: ARTICLE  
Abstract: We have isolated mutations in the gene encoding a *Drosophila* 14-3-3 epsilon protein as suppressors of the rough eye phenotype caused by the ectopic expression of RAS1(V12). Using a simple loss-of function 14-3-3 epsilon mutation, we show that 14-3-3 epsilon acts to increase the efficiency of RAS1 signaling. The 14-3-3 epsilon protein appears to function in multiple RTK pathways, suggesting that it is a general component of RAS1 signaling cascade. Sequence analysis of three dominant-negative alleles defines two regions of 14-3-3 epsilon that participate in RAS1 signaling. We also present evidence that 14-3-3 epsilon and 14-3-3 zeta, two 14-3-3 protein family members, are partially redundant for RAS1 signaling in photoreceptor formation and in animal viability. Our genetic data suggest that 14-3-3 epsilon functions downstream of or parallel to RAF, but upstream of nuclear factors in RAS1 signaling.

10/3,AB/15 Item 11 from file: 34)  
DIALOG(R) File 34 SciSearch(R) Cited Ref Sci  
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05757886 Genuine Article#: WV963 Number of References: 71  
Title: The interchain disulfide bond between TCR alpha/beta heterodimers on human T cells is not required for TCR/CD3 membrane expression and signal transduction (ABSTRACT AVAILABLE)

Author(s): Arnaud J; Hucheng A; Vernhes MC; CasparBauguil S; Lenfant F; Sancho J; Terhorst C; Rubin B (REPRINT)  
Corporate Source: CHU PURPAN, CELLULAF & MOL IMMUNOL LAB, CTR IMMUNOPATHOL & GENET HUMAINE, CIGH, CNRS/F-31300 TOULOUSE//FRANCE// (REPRINT); CHU PURPAN, CELLULAR & MOL IMMUNOL LAB, CTR IMMUNOPATHOL & GENET HUMAINE, CIGH, CNRS/F-31300 TOULOUSE//FRANCE//; CHU PURPAN, INSERM, U395/F-31300 TOULOUSE//FRANCE//; CSIC, DEPT BIOL CELLULAR & INMUNOL/GRANADA 18001//SPAIN//; HARVARD UNIV, SCH MED, BETH ISRAEL HOSP, DIV IMMUNOL/BOSTON//MA/02215

Journal: INTERNATIONAL IMMUNOLOGY, 1997, V9, N4 (APR), P615-626

ISSN: 0953-8178 Publication date: 19970400

Publisher: OXFORD UNIV PRESS, WALTON ST JOURNALS DEPT, OXFORD, ENGLAND OX2 6EP

Language: English Document Type: ARTICLE

Abstract: In the present paper, it was attempted to define the amino acids or regions on TCR beta molecules that determine the TCR alpha-TCR beta interaction. Sequence studies on HEP-ALL variant cells with an intrinsic deficiency in TCR alpha beta dimer formation elucidated a conserved amino acid motif in the TCR-C-beta beta-strand E, = Y(C)/L(S)SRLR(V)(S)(A); this motif seems to represent one interaction area for the TCR alpha-TCR beta interaction. In addition, amino acids in the connecting peptide may be shaped in a precise structure (by the interactions with CD3 molecules?) involved in TCR alpha-TCR beta dimerization. This result was supported by the finding that the interchain disulfide bond between TCR alpha and beta chains is not required for membrane expression or transmembrane signal transduction of TCR alpha beta-CD3 complexes. Finally, comparative results from two membrane TCR-CD3-negative Jurkat variants R4.9 and E6.E12 suggest that TCR-C-beta exon 1- and 5-encoded amino acids are important for the TCR beta-CD3 gamma epsilon association.

10/3,AB/16 (Item 12 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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05754761 Genuine Article# WY761 Number of References: 57  
Title: Role of CD3 gamma and CD3 delta cytoplasmic domains in cytolytic T lymphocyte functions and TCR/CD3 down-modulation (ABSTRACT AVAILABLE)

Author(s): Luton F; Buferne M; Legendre V; Chauvet E; Boyer C; SchmittVerhulst AM (REPRINT)

Corporate Source: CTR IMMUNOL, INSERM, CNRS MARSEILLE LUMINY, PARC SCI LUMINY, CASE 904 F-13288 MARSEILLE 9//FRANCE// (REPRINT); CTR IMMUNOL, INSERM, CNRS MARSEILLE LUMINY/F-13283 MARSEILLE 9//FRANCE//

Journal: JOURNAL OF IMMUNOLOGY, 1997, V158, N9 (MAY 1), P4162-4170

ISSN: 0022-1767 Publication date: 19970501

Publisher: AMER ASSOC IMMUNOLOGISTS, 9600 ROCKVILLE PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE

Abstract: TCR engagement leads to down-modulation of TCR/CD3 complexes from the T cell surface. The importance of this effect in T cell physiology is unknown. Here, we characterized a T cell clone deficient in TCR/CD3 surface expression that had lost both CD3 delta and CD3 gamma mRNA, allowing us to address the role of these chains in the assembly, signaling, and dynamics of the TCR/CD3 complex. Expression of either CD3 delta or CD3 gamma alone failed to reconstitute surface expression of the TCR/CD3 complex, but reconstitution with a cytoplasmically truncated CD3 delta (delta t) and a native (gamma) or cytoplasmically truncated (gamma t) human CD3 gamma led to reexpression of TCR/CD3 complexes in both cases. This indicated that CD3 delta and CD3 gamma assume specific functions in TCR/CD3 assembly independently of their cytoplasmic domains. The delta t gamma t variant specifically killed target cells, expressed the IFN-gamma gene in response to Ag, and produced TNF-alpha in response to anti-CD3 mAb, but it was affected in

CD3 ligand-induced TCR/CD3 down-modulation. Both PMA- and CD3 ligand-induced TCR/CD3 down-modulation were defective in the delta t gamma t variant, whereas the delta t gamma variants were unaffected, and previously described delta gamma t variants were affected only in PMA-induced down-modulation. Specific protein **kinase** C (PKC) inhibitors indicated that PMA- but not CD3 ligand-induced down-modulation was dependent on PKC activity. Thus, amino acid sequences present in either the CD3 delta or CD3 gamma cytoplasmic domain control ligand-induced TCR/CD3 down-modulation, and neither these sequences nor this property are required for cytolysis and IFN-gamma gene expression in response to Ag.

10 '3,AB/17 (Item 13 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

05533314 Genuine Article#: WE924 Number of References: 8  
Title: Purification of the T-cell receptor **zeta**-chain: Covalent modification by 4-(2-aminoethyl)benzenesulfonyl fluoride  
Author(s): Sweeney B (REPRINT) ; Proudfoot K; Parton AH; King LM; Slocombe P; Perry MJ  
Corporate Source: CELLTECH LTD,216 FATH RD/SLOUGH SL1 4EN/BERKS/ENGLAND/  
(REPRINT)  
Journal: ANALYTICAL BIOCHEMISTRY, 1997, V245, N1 (FEB 1), P107-109  
ISSN: 0003-2697 Publication date: 19970201  
Publisher: ACADEMIC PRESS INC JNL-COMP SUBSCRIPTIONS, 525 B ST, STE 1900,  
SAN DIEGO, CA 92101-4495  
Language: English Document Type: ARTICLE

10 '3,AB/18 (Item 14 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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05515605 Genuine Article#: WD587 Number of References: 25  
Title: Protein expression of the epsilon subspecies of protein **kinase** C ceases as Swiss 3T6 fibroblasts increase in cell density even though message for the protein is still present (ABSTRACT AVAILABLE)  
Author(s): Littlebury P; Watson J; Williams T; Beale G; Rumsby M (REPRINT)  
Corporate Source: UNIV YORK,DEPT BIOL/YORK YO1 5YW/N YORKSHIRE/ENGLAND/  
(PREPRINT); UNIV YORK,DEPT BIOL/YO1 5YW/N YORKSHIRE/ENGLAND/  
Journal: FEBS LETTERS, 1997, V400, N3 (JAN 6), P304-308  
ISSN: 0014-5793 Publication date: 19970106  
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS  
Language: English Document Type: ARTICLE  
Abstract: We have noted previously that growth of C6 glioma cells from low cell density to confluence and quiescence in serum is accompanied by changes in protein content of different protein **kinase** C (PKC) subspecies. Here we show that the same occurs as non-contact-inhibiting Swiss 3T6 fibroblasts grow to high density in the presence of serum. Protein expression of PKC subspecies alpha and delta increases as the cells increase in density while that of PKC-**zeta** remains the same. Unusually, protein expression of PKC-epsilon is completely down-regulated as cells grow beyond about 50% confluence and no PKC-epsilon protein can be detected in 3T6 fibroblasts at high density by Western blotting. However, mRNA for PKC-epsilon is expressed at all stages of fibroblast growth as revealed by RT-PCR. When high-density 3T6 fibroblasts are passaged to low density in fresh medium, re-expression of PKC-epsilon protein is observed within 15 min and becomes down-regulated as cells become more dense. This very rapid synthesis of PKC-epsilon is not blocked by the transcription inhibitor actinomycin D but is inhibited by cycloheximide. PKC-epsilon has some characteristics

of a novel 'early response' protein whose synthesis in newly passaged  
3T6 cells is regulated at the translational level.

?

Set	Items	Description
S1	7347	ARABIDOPSIS AND KINAS?
S2	90	S1 AND SHAGGY
S3	55	S1 AND ASK
S4	0	S1 AND DZETA
S5	21	S1 AND ZETA
S6	28	RD S2 (unique items)
S7	22	RD S3 (unique items)
S8	15	S7 NOT S6
S9	19	RD S5 (unique items)
S10	18	S9 NOT (S6 OR S7)
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	40199	ZETA
S11	73	D(W) ZETA
? s s11 and arabidopsis		
	73	S11
	95824	ARABIDOPSIS
S12	0	S11 AND ARABIDOPSIS
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\$0.43 TELNET  
\$0.43 Estimated cost this search  
\$0.43 Estimated total session cost 0.228 DialUnits

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\*File 34: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.  
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(c) 2002 CAB International  
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File 94: JICST-EPlus 1985-2002/Jun W1  
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\*File 94: There is no data missing. UDs have been adjusted to reflect the current months data. See Help News94 for details.  
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(c) 2002 The HW Wilson Co.  
File 99: Wilson Appl. Sci & Tech Abs 1983-2002/Jun  
(c) 2002 The HW Wilson Co.  
File 117: Water Resour. Abs. 1967-2002/Jun  
(c) 2002 Cambridge Scientific Abs.  
File 143: Biol. & Agric. Index 1983-2002/Jun  
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\*File 306: File has been updated & reloaded. See HELP NEWS 306. New Bluesheet available in F415 & at URL <http://library.dialog.com/bluesheets>.  
File 357: Derwent Biotech Res. 1982-2002/June W1  
(c) 2002 Thomson Derwent & ISI

\*File 357: File enhancements now online. See HELP NEWS 357.  
Alert feature enhanced for multiple files, etc. See HELP ALERT.  
File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec  
(c) 1993 Inst for Sci Info

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?	s askdzeta	
	S1	6 ASKEZETA
?	rd	
***	Duplicate detection is not supported for File 135.	
***	Duplicate detection is not supported for File 306.	
***	Records from unsupported files will be retained in the RD set.	
...	Completed examining records	
	S2	3 RD (unique items)
?	t s2/3,ab/all	
***	No matching display code(s) found in file(s): 65, 235, 306	

2,3,AB/1 (Item 1 from file 155)  
DIALOG(R) File 155: MEDLINE(R)

10165524 99178801 PMID: 10080716  
Characterization of three novel members of the *Arabidopsis* SHAGGY-related protein kinase (ASK) multigene family.

Cornelis M C; Wittich P; von Recklinghausen I; van Lammeren A; Kreis M  
Institut de Biotechnologie des Plantes - ERS/CNRS 569, Universite de Paris-Sud, Orsay, France.

Plant molecular biology (NETHERLANDS) Jan 1999, 39 (1) p137-47, ISSN 0167-4412 Journal Code: 9106343

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

In this paper we report the characterization of three novel members of the *Arabidopsis* shaggy-related protein kinase (ASK) multigene family, named **ASKdzeta** (ASKzeta), **ASKmeta** (ASKmeta) and **ASKiota** (ASKiota). The proteins encoded by the ASK genes share a highly conserved catalytic protein kinase domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase kinase-3 (GSK-3) from *Drosophila* and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in *Drosophila*. At least ten different ASK genes are expected to be present per haploid genome of *A. thaliana*. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the *Arabidopsis* genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein kinases demonstrated a clear distinction between the plant and the animal kinases. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these kinases. The differential expression patterns of five ASK genes were assessed by northern and in situ hybridization experiments using gene-specific probes. While ASKzeta is expressed in the whole embryo during its development, ASKmeta expression is limited to the suspensor cells. No signal was detected for ASKalpha, ASKgamma and ASKiota in developing embryos.

2,3,AB/2 (Item 1 from file 761)  
DIALOG(R) File 761: Life Sciences Collection  
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02559959 4495739

Characterization of three novel members of the *Arabidopsis* SHAGGY-related protein kinase (ASK) multigene family

Bornelias, M.C.; Wittich, F.; von Fecklinghausen, I.; van Lammeren, A.; Kreis, M.

Institut de Biotechnologie des Plantes ERS/CNRS 569, Université de Paris-Sud, Bâtiment 630, 91405 Orsay Cedex, France

Plant Molecular Biology vol. 39, no. 1, pp. 137-147 (1999)

ISSN: 0167-4412

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Genetics Abstracts; Biochemistry Abstracts 2: Nucleic Acids

In this paper we report the characterization of three novel members of the *Arabidopsis* shaggy-related protein kinase (ASK) multigene family, named **ASKdzeta** (ASK), **ASKetha** (ASK eta) and **ASKiota** (ASK iota). The proteins encoded by the ASK genes share a highly conserved catalytic protein kinase domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase kinase-3 (GSK-3) from *Drosophila* and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in *Drosophila*. At least ten different ASK genes are expected to be present per haploid genome of *A. thaliana*. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the *Arabidopsis* genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein kinases demonstrated a clear distinction between the plant and the animal kinases. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these kinases. The differential expression patterns of five ASK genes were assessed by northern and in situ hybridization experiments using gene-specific probes. While ASK $\gamma$  is expressed in the whole embryo during its development, ASK eta expression is limited to the suspensor cells. No signal was detected for ASK alpha, ASK gamma and ASK iota in developing embryos.

2/3,AB.3 (Item 1 from file: 144)

DISC(D) File 144:Pascal

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14249199 PASCAL No.: 99-0452372

Caractérisation d'homologues de la protéine kinase SHAGGY chez *Arabidopsis thaliana* et leur rôle biologique pendant le développement

(Characterization of *Arabidopsis thaliana* homologues of SHAGGY protein kinase and their biological role during development)

BORNELIAS Marcelo; KREIS Martin, dir

Université de Paris 11, Orsay, France

Univ.: Université de Paris 11. Orsay. FFA Degree: Th. doct.

1999-05, 1999 182 p.

Language: French Summary Language: French; English

Trois nouveaux membres de la famille multigénique ASK (pour *Arabidopsis* SHAGGY - related protein kinases) nommés **ASKdzeta** (ASK zeta), **ASKetha** (ASK eta) et **ASKiota** (ASK iota), ont été identifiés chez *Arabidopsis thaliana*. Les gènes ASK sont des homologues végétaux du gène SHAGGY (SGG) chez la *Drosophila*, appartenant à la sous-famille GSK-3 des protéines kinases. Dans un premier temps, la comparaison des séquences d'acides aminés des protéines kinases de la sous-famille GSK-3 a permis l'identification de trois groupes, évolutivement conservés, d'homologues végétaux de SGG. La comparaison des séquences nucléotidiques des gènes de la famille ASK a permis la proposition d'un modèle d'évolution de cette famille multigénique. Par la suite, l'expression des gènes ASK des groupes I et II a été étudiée pendant le développement d'*Arabidopsis* utilisant la technique d'hybridation *in situ*. Des plantes transgéniques contenant des constructions antisens des gènes ASK des groupes I et II ont été obtenues.

L'analyse des phenotypes des plantes antisens a permis la suggestion d'un role biologique pour les proteines ASK pendant le developpement floral et embryonnaire d'Arabidopsis.

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? s ask (w) dzeta not s1  
21678 ASK  
214 DZETA  
0 ASK (W) DZETA  
6 S1  
S3 0 ASK (W) DZETA NOT S1  
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e au=dornelas marcelo

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E6	10	AU=DORNELAS MC
E7	1	AU=DORNELAS, A.
E8	2	AU=DORNELAS, E.
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E11	2	AU=DORNELAS, ELLEN A
E12	3	AU=DORNELAS, G. V.

Enter P or PAGE for more

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>>> or undefined in one or more files.

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2	AU=DORNELAS MARCELO C
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10	AU=DORNELAS MC

S4 28 E1-E6

? s s4 and arabidopsis

28 S4

95824 ARABIDOPSIS

S5 12 S4 AND ARABIDOPSIS

? rd

>>>Duplicate detection is not supported for File 235.

>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.  
...completed examining records

S6 5 RD (unique items)

? t s6/3,ab/all

>>>No matching display code(s) found in file(s): 65, 235, 306

6 3,AB/1 (Item 1 from file: 155)  
DIALOG(R)File 155: MEDLINE(R)

10692832 20223136 PMID: 10758494

**Arabidopsis** thaliana SHAGGY-related protein kinases (AtSK11 and 12) function in perianth and gynoecium development.

Dornelas M C; Van Lammeren A A; Kreis M

Universite de Paris-Sud, Institut de Biotechnologie des Plantes (IBP), UMF/CNRS 8618, Batiment 630, F-91405 Orsay Cedex, France

Plant journal : for cell and molecular biology (ENGLAND) Mar 2000, 21 (3) p419-29, ISSN 0960-7412 Journal Code: 9207397

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

In higher plants, the correct patterning of the floral meristem in terms of organ type, number and form is the result of a concerted expression of a network of genes. We describe phenotypes of flower patterning, resulting from a reduction of transcript levels of the **Arabidopsis** SHAGGY-related protein kinase genes AtSK11(ASKalpha) and AtSK12(ASKgamma). The AtSK genes are plant homologues of the *Drosophila* shaggy (SGG) gene and the mammalian Glycogen-Synthase Kinase 3 (GSK-3). The SGG protein kinase is a key component of the wingless signalling pathway and is required for the

establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11(ASKalpha) and AtSK12(ASKgamma) genes during wild-type **Arabidopsis** inflorescence development, detected by *in situ* hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11(ASKalpha) and AtSK12(ASKgamma) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11(ASKalpha) and AtSK12(ASKgamma) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the apical-basal patterning of the gynoecium.

6/3,AB/2 (Item 2 from file: 155)  
DIALOG(R) File 155: MEDLINE(R)

10185524 99178801 PMID: 10080716

Characterization of three novel members of the **Arabidopsis** SHAGGY-related protein kinase (ASK) multigene family.

Dornelas M C; Wittich P; von Recklinghausen I; van Lammeren A; Freis M

Institut de Biotechnologie des Plantes ERS/CNRS 569, Universite de Paris-Sud, Orsay, France.

Plant molecular biology (NETHERLANDS) Jan 1999, 39 (1) p137-47, ISSN 0167-4412 Journal Code: 9106343

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

In this paper we report the characterization of three novel members of the **Arabidopsis** shaggy-related protein kinase (ASK) multigene family, named ASKzeta (ASKzeta), ASKeta (ASKeta) and ASK iota (ASKiota). The proteins encoded by the ASK genes share a highly conserved catalytic protein kinase domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase kinase-3 (GSK-3) from *Drosophila* and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in *Drosophila*. At least ten different ASK genes are expected to be present per haploid genome of *A. thaliana*. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein kinases demonstrated a clear distinction between the plant and the animal kinases. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these kinases. The differential expression patterns of five ASK genes were assessed by northern and *in situ* hybridization experiments using gene-specific probes. While ASKzeta is expressed in the whole embryo during its development, ASKeta expression is limited to the suspensor cells. No signal was detected for ASKalpha, ASKgamma and ASKiota in developing embryos.

6/3,AB/3 (Item 3 from file: 155)  
DIALOG(R) File 155: MEDLINE(R)

19842008 98278841 PMID: 9611268

The **Arabidopsis** SHAGGY-related protein kinase (ASK) gene family: structure, organization and evolution.

Dornelas M C; Lejeune E; Dron M; Freis M

Institut de Biotechnologie des Plantes, ERS/CNRS 569, Universite de

Paris-Sud, Batiment 630, F-91405, Orsay, Cedex, France.  
Gene (NETHERLANDS) Jun 8 1998, 212 (2) p249-57, ISSN 0378-1119  
Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Higher plants contain a multigene family encoding proteins that share a highly conserved catalytic protein kinase domain about 70% identical to SHAGGY protein kinase (SGG) and glycogen synthase kinase-3 (GSK-3), respectively, from *Drosophila* and mammals. In this study we have characterized the structure and evolution of the *Arabidopsis* SHAGGY-related protein kinase (ASK) gene family. At least ten ASK genes are present per haploid genome of *Arabidopsis*. The genomic sequences of five ASK genes show a strikingly high conservation of intron positions and exon lengths. Phylogenetic analyses suggested that the *Arabidopsis* gene family contains at least three ancient classes of genes that diverged early in land plant evolution. The different classes may reflect specificity of substrates and/or biological functions. Eight out of the ten predicted ASK genes were mapped and shown to be dispersed over the five *Arabidopsis* chromosomes. A tentative model for the organization and evolution of the *Arabidopsis* ASK genes is presented.

6/3,AB/4 (Item 1 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

10695093 Genuine Article#: 557GG Number of References: 32  
Title: A genomic approach to elucidating grass flower development (ABSTRACT AVAILABLE)

Author(s): Dornelas MC (REPRINT) ; Rodriguez APM

Corporate Source: USP,Escola Super Agr Luiz de Queiroz, Dept Ciencias Florestais,Av Padua Dias 11/BR-13418900 Piracicaba/SP/Brazil/ (REPRINT) ; USP,Escola Super Agr Luiz de Queiroz, Dept Ciencias Florestais, BR-13418900 Piracicaba/SP/Brazil/; USP,Ctr Energia Nucl Agr, Lab Biotecnol Vegetal,BF-13400970 Piracicaba/SP/Brazil/

Journal: GENETICS AND MOLECULAR BIOLOGY, 2001, V24, N1-4, P69-76

ISSN: 1415-4757 Publication date: 20010000

Publisher: SOC BRASIL GENETICA, RUA CAP ADELMIC NORBET DA SILVA, 736, ALTO DA BOA VISTA, 14025-670 RIBEIRAO PRET, BRAZIL

Language: English Document Type: ARTICLE

Abstract: In sugarcane (*Saccharum* sp) as with other species of grass, at a certain moment of its life cycle the vegetative meristem is converted into an inflorescence meristem which has at least two distinct inflorescence branching steps before the spikelet meristem terminates in the production of a flower (floret). In model dicotyledonous species such successive conversions of meristem identities and the concentric arrangement of floral organs in specific whorls have both been shown to be genetically controlled. Using data from the Sugarcane Expressed Sequence Tag (EST) Project (SUCEST) database, we have identified all sugarcane proteins and genes putatively involved in reproductive meristem and flower development. Sequence comparisons of known flower-related genes have uncovered conserved evolutionary pathways of flower development and flower pattern formation between dicotyledons and monocotyledons, such as some grass species. We have paid special attention to the analysis of the MADS-box multigene family of transcription factors that together with the APETALA2 (AF2) family are the key elements of the transcriptional networks controlling plant reproductive development. Considerations on the evolutionary developmental genetics of grass flowers and their relation to the ABC homeotic gene activity model of flower development are also presented.

6/3,AB/5 (Item 1 from file: 144)  
DIALOG(R) File 144:Pascal  
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14249399 PASCAL No.: 99-0452372  
Caracterisation d'homologues de la proteine kinase SHAGGY chez  
**Arabidopsis** thaliana et leur role biologique pendant le developpement  
(Characterization of **Arabidopsis** thaliana homologues of SHAGGY  
protein kinase and their biological role during development)

DORNELAS Marcelo; KREIS Martin, dir  
Universite de Paris 11, Orsay, France  
Univ.: Universite de Paris 11. Orsay. FRA Degree: Th. doct.  
1999-05; 1999 182 p.

Language: French Summary Language: French; English  
Trois nouveaux membres de la famille multigenique ASK (pour  
**Arabidopsis** SHAGGY - related protein kinases) nommés ASK $\zeta$  (ASK zeta), ASK $\eta$  (ASK eta) et ASK $\iota$  (ASK iota), ont été identifiés chez **Arabidopsis** thaliana. Les gènes ASK sont des homologues végétaux du gène SHAGGY (SGG) chez la *Drosophila*, appartenant à la sous-famille GSK-3 des protéines kinases. Dans un premier temps, la comparaison des séquences d'acides aminés des protéines kinases de la sous-famille GSK-3 a permis l'identification de trois groupes, évolutivement conservés, d'homologues végétaux de SGG. La comparaison des séquences nucléotidiques des gènes de la famille ASK a permis la proposition d'un modèle d'évolution de cette famille multigenique. Par la suite, l'expression des gènes ASK des groupes I et II a été étudiée pendant le développement d'**Arabidopsis** utilisant la technique d'hybridation *in situ*. Des plantes transgéniques contenant des constructions antisens des gènes ASK des groupes I et II ont été obtenues. L'analyse des phénotypes des plantes antisens a permis la suggestion d'un rôle biologique pour les protéines ASK pendant le développement floral et embryonnaire d'**Arabidopsis**.

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ds

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S2	3	RD (unique items)
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S4	28	E1-E6
S5	12	S4 AND AFABIDOPSIS
S6	5	RD (unique items)

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e au=van lammeren, andre

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E10	3	AU=VAN LAMMEREN, JOOP P. M
E11	7	AU=VAN LAMMEREN, M.
E12	1	AU=VAN LAMMEREN, P.

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1	AU=VAN LAMMEREN, ANDRE C. A. P

S9 17 E1-E5

? s s9 and arabidopsis

17	S9
95824	ARABIDOPSIS
S10	2 S9 AND ARABIDOPSIS

? rd

>>>Duplicate detection is not supported for File 235.

>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.

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>>>No matching display code(s) found in file(s): 65, 235, 306

11 3,AB/1 (Item 1 from file: 76:  
DIALOG(F)File 76:Life Sciences Collection  
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02705721 5357176

Condensin and cohesin knockouts in **Arabidopsis** exhibit a titan seed phenotype

Liu, Chun ming; McElver, J.; Tzafrir, I.; Joosen, R.; Wittich, P.; Patton, D.; **Van Lammeren, A.A.M.**; Meinke, D.

Department of Botany, Oklahoma State University, Stillwater, OK 74078, USA  
Plant Journal vol. 29, no. 4, pp. 405-415 (2002)

ISSN: 0960-7412

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Genetics Abstracts

The titan (ttn) mutants of **Arabidopsis** exhibit striking alterations in chromosome dynamics and cell division during seed development. Endosperm defects include aberrant mitoses and giant polyploid nuclei. Mutant embryos differ in cell size, morphology and viability, depending on the locus involved. Here we demonstrate that three TTN genes encode chromosome scaffold proteins of the condensin (SMC2) and cohesin (SMC1 and SMC3) classes. These proteins have been studied extensively in yeast and animal systems, where they modulate chromosome condensation, chromatid separation, and dosage compensation. **Arabidopsis** contains

single copies of SMC1 and SMC3 cohesins. We used forward genetics to identify duplicate T-DNA insertions in each gene. These mutants (ttn7 and ttn8) have similar titan phenotypes: giant endosperm nuclei and arrested embryos with a few small cells. A single SMC2 knockout (ttn3) was identified and confirmed by molecular complementation. The weak embryo phenotype observed in this mutant may result from expression of a related gene (AtSMC2) with overlapping functions. Further analysis of titan mutants and the SMC gene family in **Arabidopsis** should provide clues to chromosome mechanics in plants and insights into the regulation of nuclear activity during endosperm development.

11/3,AB/2 (Item 2 from file: 76)  
DIALOG(F)File 76:Life Sciences Collection  
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02479619 4699031  
**Arabidopsis** thaliana SHAGGY-related protein kinases (AtSK11 and 12)  
function in perianth and gynoecium development  
Dornelas, M.C.; **van Lammeren, A.A.M.**; Kreis, M.  
Universite de Paris-Sud, Institut de Biotechnologie des Plantes (IBP),  
UMR/CNRS 8618, Batiment 630, F-91405 Orsay Cedex, France  
Plant Journal vol. 21, no. 5, pp. 419-429 (2000)  
ISSN: 0960-7412  
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH  
SUBFILE: Genetics Abstracts

In higher plants, the correct patterning of the floral meristem in terms of organ type, number and form is the result of a concerted expression of a network of genes. We describe phenotypes of flower patterning, resulting from a reduction of transcript levels of the **Arabidopsis** SHAGGY-related protein kinase genes AtSK11(ASK alpha) and AtSK12(ASK gamma). The AtSK genes are plant homologues of the *Drosophila* shaggy (SGG) gene and the mammalian Glycogen-Synthase Kinase-3 (GSK-3). The SGG protein kinase is a key component of the wingless signalling pathway and is required for the establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11(ASK alpha) and AtSK12(ASK gamma) genes during wild-type **Arabidopsis** inflorescence development, detected by *in situ* hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11(ASK alpha) and AtSK12(ASK gamma) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11(ASK alpha) and AtSK12(ASK gamma) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the apical-basal patterning of the gynoecium.

?

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E8	1	AU=VANLAMMEEPEI F M
E9	7	AU=VANLAMMEEPEI FM
E10	2	AU=VANLAMMEREN J
E11	5	AU=VANLAMMEREN JPM
E12	1	AU=VANLAMMEREN R

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? s e3-e6

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S12 83 E3-E6

? s s12 and arabidopsis

83	S12
95824	ARABIDOPSIS
S13	4 S12 AND ARABIDOPSIS

? rd

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>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.

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S15	4 S14 NOT 11

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15/3,AE/1 (Item 1 from file: 34)  
DIALOG(P) File 34:SciSearch(R) Cited Ref Sci  
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08663974 Genuine Article#: 313JP Number of References: 31

Title: Structure and development of somatic embryos formed in  
**Arabidopsis** thaliana pt mutant callus cultures derived from  
seedlings (ABSTRACT AVAILABLE)

Author(s): vonRecklinghausen IR; Iwanowska A; Kieft H; Mordhorst AP; Schel  
JHN; **vanLammeren AAM (REPRINT)**

Corporate Source: WAGENINGEN UNIV AGR,LAB EXPT MORPHOL & CELL BIOL,  
ARBORETUMLAAN 4/NL-6703 BD WAGENINGEN//NETHERLANDS/ (REPRINT);  
WAGENINGEN UNIV AGR,LAB EXPT MORPHOL & CELL BIOL/NL-6703 BD  
WAGENINGEN//NETHERLANDS/; WAGENINGEN UNIV AGR,MOL BIOL LAB/NL-6703 BD  
WAGENINGEN//NETHERLANDS/

Journal: PROTOPLASMA, 2000, V211, N3-4, P217-224

ISSN: 0033-183X Publication date: 20000000

Publisher: SPRINGER-VERLAG WIEN, SACHSENPLATZ 4-6, PO BOX 89, A-1201  
VIENNA, AUSTRIA

Language: English Document Type: ARTICLE

Abstract: Seeds of the **Arabidopsis** thaliana mutant primordia timing

(pt) were germinated in 2,4-dichlorophenoxyacetic acid-containing liquid medium. The seedlings formed somatic embryos and nonembryogenic and embryogenic callus in vitro in a time period of approximately two to three weeks. Embryogenesis and callus formation were monitored with respect to origin, structure, and development. Ten days after germination globular structures appeared in close vicinity of and on the shoot apical meristem (SAM). Somatic embryos formed either directly on the SAM region of the seedling or indirectly on embryogenic callus that developed at the SAM zone. Globular structures developed along the vascular tissue of the cotyledons as well, but only incidentally they formed embryos. Upon deterioration, the cotyledons formed callus. Regular subculture of the embryogenic callus gave rise to high numbers of somatic embryos. Such primary somatic embryos, grown on callus, originated from meristematic cell clusters located under the surface of the callus. Embryos at the globular and heart-shape stage were mostly hidden within the callus. Embryos at torpedo stage appeared at the surface of the callus because their axis elongated. Secondary somatic embryos frequently formed directly on primary ones. They preferentially emerged from the SAM region of the primary somatic embryos, from the edge of the cotyledons, and from the hypocotyl. We conclude that the strong regeneration capacity of the pt mutant is based on both recurrent and indirect embryogenesis.

15/3,AB/2 (Item 2 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
(c) 2002 Inst for Sci Info. All rts. reserv.

08560880 Genuine Article# 300TZ Number of References: 51  
Title: **Arabidopsis** thaliana SHAGGY-related protein kinases (AtSK11 and 12) function in perianth and gynoecium development (ABSTRACT AVAILABLE)  
Author(s): Dornelas MC; **vanLammeren AAM**; Kreis M (REPRINT)  
Corporate Source: UNIV PARIS 11,INST BIOTECHNOL PLANTES, CNRS, UMR 8618, BATIMENT 630/F-91405 ORSAY//FRANCE (REPRINT); UNIV PARIS 11,INST BIOTECHNOL PLANTES, CNRS, UMR 8618, F-91405 ORSAY//FRANCE//; AGR UNIV WAGENINGEN,LAB EXPT PLANT MORPHOL & CELL BIOL/NL-6703 BD WAGENINGEN//NETHERLANDS/

Journal: PLANT JOURNAL, 2000, V21, N5 MAR, P419-429  
ISSN: 0960-7412 Publication date: 20000300  
Publisher: BLACKWELL SCIENCE LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 0NE, OXON, ENGLAND

Language: English Document Type: ARTICLE

Abstract: In higher plants, the correct patterning of the floral meristem in terms of organ type, number and form is the result of a concerted expression of a network of genes. We describe phenotypes of flower patterning, resulting from a reduction of transcript levels of the **Arabidopsis** SHAGGY-related protein kinase genes AtSK11 (ASK alpha) and AtSK12 (ASK gamma). The AtSK genes are plant homologues of the *Drosophila* shaggy (SGG) gene and the mammalian Glycogen-Synthase Kinase-3 (GSK-3). The SGG protein kinase is a key component of the wingless signalling pathway and is required for the establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11 (ASK alpha) and AtSK12 (ASK gamma) genes during wild-type **Arabidopsis** inflorescence development, detected by in situ hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11 (ASK alpha) and AtSK12 (ASK gamma) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11 (ASK alpha) and AtSK12 (ASK gamma) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the

apical-basal patterning of the gynoecium.

15/3,AB/3 (Item 3 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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08315-11 Genuine Article#: 270KW Number of References: 37  
Title: beta-tubulin accumulation and DNA synthesis are sequentially resumed in embryo organs of cucumber (*Cucumis sativus L.*) seeds during germination (ABSTRACT AVAILABLE)  
Author(s): Jing HC; **vanLammeren AAM**; deCastro RD; Bino RJ; Hilhorst HWM; Groot SPC (REPRINT)  
Corporate Source: CTR PLANT BREEDING & REPROD RES,AGR RES DEPT, POSTBUS 16/NL-6700 AA WAGENINGEN//NETHERLANDS/ (REPRINT); CTR PLANT BREEDING & REPROD RES,AGR RES DEPT/NL-6700 AA WAGENINGEN//NETHERLANDS/; WAGENINGEN UNIV AGR,LAB PLANT CYTOL & MORPHOL/WAGENINGEN//NETHERLANDS/; WAGENINGEN UNIV AGR,LAB PLANT PHYSIOL/WAGENINGEN//NETHEPLANDS/; TIANJIN ACAD AGR SCI, /TIANJIN//PEOPLES R CHINA/  
Journal: PROTOPLASMA, 1999, V208, N1-4, P230-239  
ISSN: 0033-183X Publication date: 19990000  
Publisher: SPRINGER-VERLAG WIEN, SACHSENPLATZ 4-6, PO BOX 89, A-1201 VIENNA, AUSTRIA  
Language: English Document Type: ARTICLE  
Abstract: Resumption of DNA synthetic activities and beta-tubulin accumulation was studied in embryo organs of germinating cucumber (*Cucumis sativus L.*) seeds. Flow-cytometric analysis indicated the existence of 2C, 4C, and 8C nuclei in the radicle of mature embryos, whereas in cotyledons most of the cells contained nuclei with 2C DNA content. Upon imbibition of water, nuclear DNA replication was initiated in the radicle within 15 h, subsequently spreading towards the cotyledons. Bromodeoxyuridine incorporation preceded detectable changes in the relative amounts of DNA, implying the occurrence of putative DNA repair. Organellar DNA synthesis occurred independently of the nuclear DNA synthetic cycle. Western blotting and immunohistochemical localization demonstrated that the constitutive level of beta-tubulin originated from preserved P-tubulin granules. During imbibition, disappearance of fluorescent tubulin granules, accumulation of beta-tubulin, and formation of microtubular cytoskeleton were found in the radicle, but not in the cotyledon areas. Mitosis only occurred after radicle protrusion at 21 h of imbibition. It is concluded that the differences in the initiation and progress of these cellular and molecular events are associated with the discrete behaviors of the radicle and the cotyledons upon imbibition. The formation of cortical microtubular cytoskeleton and the accumulation of tubulins are important features in preparation of radicle protrusion, whereas DNA synthesis may contribute to postgerminative growth.

15/3,AB/4 (Item 4 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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07489949 Genuine Article#: 172TE Number of References: 53  
Title: Characterization of three novel members of the **Arabidopsis** SHAGGY-related protein kinase (ASK) multigene family (ABSTRACT AVAILABLE)  
Author(s): Dornelas MC; Wittich P; vonRecklinghausen I; **vanLammeren A** : Kreis M (REPRINT)  
Corporate Source: UNIV PARIS 11,INST BIOTECHNOL PLANTES, EFS CNRS 569, FRATIMENT 630/F-91405 CRSAY//FRANCE/ (REPRINT); UNIV PARIS 11,INST BIOTECHNOL PLANTES, EFS CNRS 569/F-91405 DRSAY//FRANCE/; AGR UNIV WAGENINGEN,LAB PLANT CYTOL & MORPHOL/NL 6703 BD WAGENINGEN//NETHERLANDS/

Journal: PLANT MOLECULAR BIOLOGY, 1999, V39, N1 (JAN), P137-147  
ISSN: 0167-4412 Publication date: 19990100  
Publisher: KLUWER ACADEMIC PUBL, SPUIBOULEVARD 50, PO BOX 17, 3300 AA  
DOORDRECHT, NETHERLANDS

Language: English Document Type: ARTICLE

Abstract: In this paper we report the characterization of three novel members of the *Arabidopsis* shaggy-related protein kinase (ASK) multigene family, named ASK $\zeta$  (ASK zeta), ASK $\eta$  (ASK eta) and ASK $\iota$  (ASK iota). The proteins encoded by the ASK genes share a highly conserved catalytic protein kinase domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase kinase-3 (GSK-3) from *Drosophila* and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in *Drosophila*. At least ten different ASK genes are expected to be present per haploid genome of *A. thaliana*. Different amino- and carboxy-terminal extensions distinguish different ASK family members. Five ASK gene sequences were analysed and shown to be present as single-copy genes in the *Arabidopsis* genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein kinases demonstrated a clear distinction between the plant and the animal kinases. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these kinases. The differential expression patterns of five ASK genes were accessed by northern and *in situ* hybridization experiments using gene-specific probes. While ASK zeta is expressed in the whole embryo during its development, ASK eta expression is limited to the suspensor cells. No signal was detected for ASK alpha, ASK gamma and ASK iota in developing embryos.

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E2	2	AU=KREIS M F
E3	38	*AU=KREIS MARTIN
E4	19	AU=KREIS MARTIN E
E5	54	AU=KREIS ME
E6	3	AU=KREIS N
E7	2	AU=KREIS NADJA
E8	3	AU=KREIS O
E9	77	AU=KREIS P
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E11	3	AU=KREIS PETER
E12	1	AU=KREIS PETR

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54	AU=KREIS ME

S16 175 E1-E5

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95824	ARABIDOPSIS

S17 30 S16 AND ARABIDOPSIS

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30	S17
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0	S3
28	S4
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4	S13
4	S14
4	S15
175	S16

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Set	Items	Description
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S6	5	RD (unique items)
S7	28	E4-E9
S8	0	S7 NOT S4
S9	17	E1-E5
S10	2	S9 AND ARABIDOPSIS
S11	2	RD (unique items)

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21678 ASK  
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21'3,AB/1 (Item 1 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
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12473728 BIOSIS NO.: 200000227230  
**Arabidopsis thaliana** SHAGGY-related protein kinases (AtSK11 and 12)  
function in perianth and gynoecium development.  
AUTHOR: Dornelas Marcelo C; van Lammeren Andie AM; **Kreis Martin**(a  
AUTHOR ADDRESS: (a)Institut de Biotechnologie des Plantes (IBP), UMR/CNRS  
8616, Universite de Paris-Sud, Batiment 630, F-91405, Orsay\*\*France  
JOURNAL: Plant Journal 21 (5):p419-429 March, 2000  
ISSN: 0960-7412  
DOCUMENT TYPE: Article  
RECORD TYPE: Abstract  
LANGUAGE: English  
SUMMARY LANGUAGE: English

ABSTRACT: In higher plants, the correct patterning of the floral meristem in terms of organ type, number and form is the result of a concerted expression of a network of genes. We describe phenotypes of flower patterning, resulting from a reduction of transcript levels of the **Arabidopsis** SHAGGY-related protein kinase genes AtSK11(**ASKalpha**) and AtSK12(**ASKalpha**). The AtSK genes are plant homologues of the *Drosophila* shaggy (SGG) gene and the mammalian Glycogen-Synthase Kinase-3 (GSK-3). The SGG protein kinase is a key component of the wingless signalling pathway and is required for the establishment of tissue patterning and cell fate determination. The expression patterns of the AtSK11(**ASKalpha**) and AtSK12(**ASKgamma**) genes during wild-type **Arabidopsis** inflorescence development, detected by *in situ* hybridisation, have been shown to be consistent with a possible role in floral meristem patterning. AtSK11(**ASKalpha**) and AtSK12(**ASKgamma**) transcripts were detected at the periphery of the inflorescence meristem and in the floral meristem. At later stages the expression of the AtSK genes became localised in specific regions of developing flower organ primordia. Furthermore, we have obtained and analysed transgenic plants containing AtSK11(**ASKalpha**) and AtSK12(**ASKgamma**) gene specific antisense constructs. These plants developed flowers showing a higher number of perianth organs and an alteration of the apical-basal patterning of the

gynoecium.

2000

21/3,AB/2 (Item 2 from file: 5)  
DIALOG(R) File 5:Biosis Previews(R)  
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11928692 BIOSIS NO.: 199900174801  
Characterization of three novel members of the **Arabidopsis**  
SHAGGY-related protein kinase (**ASK**) multigene family.  
AUTHOR: Dornelas Marcelo; Carnier; Wittich Peter; von Recklinghausen Iris;  
van Lammeren Andre; **Kreis Martin**(a)  
AUTHOR ADDRESS: (a)Institut de Biotechnologie des Plantes ERS/CNRS 569,  
Universite de Paris-Sud, Batiment 630, 9140\*\*France  
JOURNAL: Plant Molecular Biology 39 (1):p137-147 Jan., 1999  
ISSN: 0167-4412  
DOCUMENT TYPE: Article  
RECORD TYPE: Abstract  
LANGUAGE: English

ABSTRACT: In this paper we report the characterization of three novel members of the **Arabidopsis** shaggy-related protein kinase (**ASK**) multigene family, named **ASKdzeta** (**ASKzeta**), **ASKetha** (**ASKeta**) and **ASKiota** (**ASKiota**). The proteins encoded by the **ASK** genes share a highly conserved catalytic protein kinase domain and show about 70% identity to SHAGGY (SGG) and glycogen synthase kinase-3 (GSK-3) from *Drosophila* and rat respectively. SGG is an ubiquitous intracellular component of the wingless signalling pathway that establishes cell fate and/or pattern formation in *Drosophila*. At least ten different **ASK** genes are expected to be present per haploid genome of *A. thaliana*. Different amino- and carboxy-terminal extensions distinguish different **ASK** family members. Five **ASK** gene sequences were analysed and shown to be present as single-copy genes in the **Arabidopsis** genome. A comparison based on the highly conserved catalytic domain sequences of all known sequences of the GSK-3 subfamily of protein kinases demonstrated a clear distinction between the plant and the animal kinases. Furthermore, we established the presence of at least three distinct groups of plant homologues of SGG/GSK-3. These different groups probably reflect biochemical and/or biological properties of these kinases. The differential expression patterns of five **ASK** genes were accessed by northern and in situ hybridization experiments using gene-specific probes. While **ASKzeta** is expressed in the whole embryo during its development, **ASKeta** expression is limited to the suspensor cells. No signal was detected for **ASKalpha**, **ASKgamma** and **ASKiota** in developing embryos.

1999

21/3,AB/3 (Item 3 from file: 5)  
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11537315 BIOSIS NO.: 199800318647  
The **Arabidopsis** SHAGGY-related protein kinase (**ASK**) gene  
family: Structure, organization and evolution.  
AUTHOR: Dornelas Marcelo; Carnier; Lejeune Bernard; Dron Michel; **Kreis Martin**(a)  
AUTHOR ADDRESS: (a)Inst. Biotechnol. Plantes, ERS/CNRS 569, Univ.  
Paris-Sud, Batiment 630, F-91405 Orsay Cedex\*\*France  
JOURNAL: Gene (Amsterdam) 212 (2):p249-257 June 8, 1998  
ISSN: 0378-1119

DOCUMENT TYPE: Article  
RECORD TYPE: Abstract  
LANGUAGE: English

ABSTRACT: Higher plants contain a multigene family encoding proteins that share a highly conserved catalytic protein kinase domain about 70% identical to SHAGGY protein kinase (SGG) and glycogen synthase kinase-3 (GSK-3), respectively, from *Drosophila* and mammals. In this study we have characterized the structure and evolution of the **Arabidopsis** SHAGGY-related protein kinase (ASK) gene family. At least ten ASK genes are present per haploid genome of **Arabidopsis**. The genomic sequences of five ASK genes show a strikingly high conservation of intron positions and exon lengths. Phylogenetic analyses suggested that the **Arabidopsis** gene family contains at least three ancient classes of genes that diverged early in land plant evolution. The different classes may reflect specificity of substrates and/or biological functions. Eight out of the ten predicted ASK genes were mapped and shown to be dispersed over the five **Arabidopsis** chromosomes. A tentative model for the organization and evolution of the **Arabidopsis** ASK genes is presented.

1998

21/3,AB/4 (Item 4 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
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09164576 BIOSIS NO.: 199497172946  
**Arabidopsis** homologs of the shaggy and GSK-3 protein kinases: Molecular cloning and functional expression in *Escherichia coli*.  
AUTHOR: Bianchi Michele W(a); Guivarc'h Dominique; Thomas Martine; Woodgett James R; **Kreis Martin**  
AUTHOR ADDRESS: (a) Biol. Dev. Plantes, Centre Recherches sur les Plantes, URA 1128, Univ. Paris-Sud, Bat. 430, F-91\*\*France  
JOURNAL: Molecular & General Genetics 242 (3):p337-345 1994  
ISSN: 0026-8925  
DOCUMENT TYPE: Article  
RECORD TYPE: Abstract  
LANGUAGE: English

ABSTRACT: The conservation in evolution of fundamental signal transduction modules offers a means of isolating genes likely to be involved in plant development. We have amplified by PCR **Arabidopsis** cDNA and genomic sequences related to the product of the shaggy/zeste-white 3 (sgg) segment polarity gene of *Drosophila*. This regulatory protein is functionally homologous to glycogen synthase kinase-3 in mammals (GSK-3), which regulates, among others, the DNA-binding activity of the c-jun/AP1 transcription factor. Analysis of PCR products led to the identification of five genes; for two of which, corresponding full-length cDNAs, ASK-alpha and gamma (for **Arabidopsis** shaggy-related protein kinase), were characterized. The encoded proteins were 70% identical to GSK-3 and sgg over the protein kinase catalytic domain and, after production in *Escherichia coli*, autophosphorylated mainly on threonine and serine residues, but phosphorytyrosine was also detected. ASK-alpha and ASK-gamma also phosphorylated phosphatase inhibitor-2 and myelin basic protein, on threonine and serine, respectively. The high conservation of the protein kinases of GSK-3 family, and their action at the transcriptional level, suggest that the ASK proteins have important functions in higher plants.

1994

21/3,AB/5 (Item 1 from file: 144)

DIALOG(R)File 144:Pascal

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14249399 PASCAL No.: 99-0452372

Caracterisation d'homologues de la proteine kinase SHAGGY chez **Arabidopsis thaliana** et leur role biologique pendant le developpement  
(Characterization of **Arabidopsis thaliana** homologues of SHAGGY protein kinase and their biological role during development)

DOFNELAS Marcelo; **KREIS Martin**, dir

Universite de Paris 11, Orsay, Francee

Univ.: Universite de Paris 11. Orsay. FRA Degree: Th. doct.

1999-05; 1999 182 p.

Language: French Summary Language: French; English

Trs nouveaux membres de la famille multigenique **ASK** (pour **Arabidopsis SHAGGY** - related protein kinases) nommes **ASKdzeta** (

**ASK zeta**), **ASKetha** (**ASK eta**) et **ASKiota** (

**ASK iota**), ont ete identifies chez **Arabidopsis thaliana**. Les

genes **ASK** sont des homologues vegetaux du gene SHAGGY (SGG) chez la *Drosophila*, appartenant a la sous-famille GSK-3 des protein kinases. Dans un premier temps, la comparaison des sequences d'acides amines des protein kinases de la sous-famille GSK-3 a permis l'identification de trois groupes, evolutivement conserves, d'homologues vegetaux de SGG. La comparaison des sequences nucleotidiques des genes de la famille **ASK** a permis la proposition d'un modele d'evolution de cette famille multigenique. Par la suite, l'expression des genes **ASK** des groupes I et II a ete etudiee pendant le developpement d'**Arabidopsis** utilisant la technique d'hybridation in situ. Des plantes transgeniques contenant des constructions antisens des genes **ASK** des groupes I et II ont ete obtenues. L'analyse des phenotypes des plantes antisens a permis la suggestion d'un role biologique pour les protein kinases **ASK** pendant le developpement floral et embryonnaire d'**Arabidopsis**.

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21/3,AB/6 (Item 2 from file: 144)

DIALOG(R)File 144:Pascal

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11433753 PASCAL No.: 94-0267915

Isollement et caracterisation d'homologues de la proteine kinase shaggy/GSK-3 chez **Arabidopsis thaliana** et identification d'un gene correspondant chez *Saccharomyces cerevisiae*

Isolation and characterization of **Arabidopsis thaliana** homologs of the shaggy/gsk-3 protein kinase and identification of a corresponding gene in *Saccharomyces cerevisiae*)

BIANCHI Michele; **KREIS Martin**, dir

Universite de Paris 11, Francee

Univ.: Universite de Paris 11. FRA Degree: Th. doct.

1993-09; 1993 155 p.

Language: French Summary Language: French; English

Les protein kinases (PKs) sont les composants centraux du systeme cybernetique des cellules eucaryotes. L'identification d'homologues de PKs conservees au cours de l'evolution peut constituer une approche complementaire aux techniques genetiques pour l'etude de voies de transduction importantes chez les plantes. Dans un premier temps, une approche de PCR (polymerase chain reaction) a permis d'identifier, chez **Arabidopsis thaliana**, une famille de genes apparentes a (1) MCK1 (meiosis and centromere regulatory kinase) de *Saccharomyces cerevisiae*; (2) shaggy/zeste-white 3, impliquee dans le developpement de *Drosophila melanogaster*; (3) le gene codant la glycogen synthase kinase-3 (GSK-3, regulateur du facteur transcriptionnel c-Jun) de mammiferes. Par la suite, la caracterisation de deux ADNs, **ASK** alpha et **ASK**-gamma (

**Arabidopsis** shaggy-related protein kinase), a permis de mettre en evidence une identite de 70%, au niveau du domaine catalytique, entre les proteines **ASK** et shaggy/GSK-3 dont ils representent donc les homologues vegetaux. L'activite kinase ainsi qu'une autophosphorylation sur des residus threonine, serine et, en plus faible quantite, tyrosine, ont pu etre demontrées apres production des proteines **ASK** dans *E. coli*. Par ailleurs, le niveau relativement faible d'identite avec MCK1 (40%) a mene a la recherche puis a l'isolement d'un deuxième gene de *S. cerevisiae*: ScGSK-3, dont le produit putatif est identique a 60%, au niveau du domaine catalytique, avec GSK-3, shaggy et les proteines **ASK**. Une analyse de phylogenie moleculaire a suggere que ScGSK-3 code le véritable homologue de GSK-3 et shaggy, alors que MCK1 serait originaire d'un evenement de duplication specifique du lignage de *S. cerevisiae*. L'etude simultanee des PKs de la famille GSK-3 dans differents organismes devrait fournir une aide importante a la comprehension des fonctions biochimiques et biologiques des proteines **ASK** chez les plantes superieures

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95824 ARABIDOPSIS  
S1 315 TRANSFORM? AND REVIEW? AND ARABIDOPSIS

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4,3,AB/1 (Item 1 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
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13549432 BIOSIS NO.: 200200178253  
**Arabidopsis:** A laboratory manual.  
BOOK TITLE: **Arabidopsis:** A laboratory manual  
AUTHOR: Weigel Detlef(a); Glazebrook Jane  
BOOK AUTHOR/EDITOR: Weigel Detlef; Glazebrook Jane: Eds  
AUTHOR ADDRESS: (a)Plant Biology Laboratory, Salk Institute, La Jolla, CA\*\*  
USA  
p: xdi; 1-354 2002  
MEDIUM: print  
BOOK PUBLISHER: Cold Spring Harbor Laboratory Press, 500 Sunnyside  
Boulevard, Woodbury, NY, 11797-2924, USA  
ISBN: 0-87969-572-2 (cloth)  
DOCUMENT TYPE: Book  
RECORD TYPE: Abstract  
LANGUAGE: English

ABSTRACT: This manual contains techniques for working with  
**Arabidopsis** that have been assembled and **reviewed** by two  
members of the plant research community. In these eight chapters, the  
authors provide step-by-step guides on growth, obtaining mutants, genetic  
analysis, **transforming Arabidopsis**, isolating genes, studying  
gene expression and studying gene function. Each chapter includes  
bibliographical references. Appendices on where to find information,

statistics tables, cautions, and suppliers are included. An index is also included at the back of the book.

2002

4/3,AB/2 (Item 2 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
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13059554 BIOSIS NO.: 200100265703  
Transgenesis of **Arabidopsis thaliana** for understanding plant gene structure and functions.

AUTHOR: Ondrej Milcs(a)

AUTHOR ADDRESS: (a)Institute of Plant Molecular Biology, Academy of Sciences of the Czech Republic, Branisovska 31, CZ-37005, Ceske Budejovice\*\*Czech Republic

JOURNAL: Biologia (Bratislava) 56 (1):p1-5 February, 2001

MEDIUM: print

ISSN: 0006-3088

DOCUMENT TYPE: Literature Review

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: Insertion mutagenesis of **Arabidopsis thaliana** is reviewed as efficient means to clone genes known only by phenotype and to correlate gene sequence and function. Random insertions of T-DNA or modified maize transposons introduced into *A. thaliana* genome by *Agrobacterium tumefaciens* lead to mutations. The mutation sites are tagged by the T-DNA or modified transposon sequences and they can be cloned by plasmid rescue or iPCR. In order to have 95% probability of hitting all *A. thaliana* genes, 100 000 independent insertion lines should be induced and this number has already been nearly reached. Only minority of insertion mutations are connected with distinct phenotypic effect, but all insertion mutations in the chosen gene sequence can be selected by pooling insertion lines and utilization of combination of direct and reverse genetic attitudes.

2001

4/3,AB/3 (Item 1 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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09716923 Genuine Article#: 441TU Number of References: 199  
Title: Superfluous transgene integration in plants (ABSTRACT AVAILABLE)  
Author(s): Smith N (REPRINT); Kilpatrick JS; Whitelam GC  
Corporate Source: ADAS Nutr Sci Res Unit,Leicester Rd/Stratford Upon Avon CV3 7 9RQ//England/ (REPRINT); ADAS Nutr Sci Res Unit,Stratford Upon Avon CV3 7 9RQ//England/; ADAS Rosemaund,Hereford HR1 3PG//England/; Univ Leicester,Dept Biol,Leicester LE1 7RH/Leics/England/

Journal: CRITICAL REVIEWS IN PLANT SCIENCES, 2001, V20, N3, P215-249  
ISSN: 0735-2639 Publication date: 20010000

Publisher: CRC PRESS LLC, 2000 CORPORATE BLVE NW, JOURNALS CUSTOMER SERVICE, BOCA RATON, FL 33431 USA

Language: English Document Type: REVIEW

Abstract: Recent reports suggest the transfer of superfluous DNA sequences to plant genomes during transformation processes. This review investigates the evidence from the published literature for the prevalence of this phenomenon and highlights methods to limit or prevent DNA transfer and subsequent potentially detrimental evolutionary consequences.

Evidence for superfluous foreign DNA transfer using both Agrobacterium-mediated **transformation** and direct DNA transfer methods such as microprojectile bombardment and PEG-mediated **transformation** of protoplasts is reported. In the case of Agrobacterium-mediated **transformation**, the lack of information on the integration of sequences from outside of the T-DNA borders has been due to the general belief by researchers that T-DNA processing is precise. This assumption was based on analysis of T-DNA in tumors and as a result the majority of T-DNA integration events have been identified exclusively using DNA probes, which are homologous only to DNA from within the T-DNA borders. Where direct gene transfer protocols are employed, any part of the **transforming** plasmid and indeed accompanying carrier DNA may become integrated into the plant genome. The main body of evidence proving that superfluous **vector** DNA sequences are present in plant genomes **transformed** using direct transfer methods is confined to the identification of plasmid concatamers integrated into plant genomes.

The limited amount of recorded evidence pertaining to superfluous **vector** DNA integration in transgenic plants and **transformed** tissues makes it impossible to draw definitive conclusions as to the factors involved in promoting this phenomenon. However, there are methods available for removing superfluous sequences from transgenic plants. These have been developed for the removal of selectable marker genes, whose presence in transgenic plants has been a source of much controversy, but can equally be applied to other DNA sequences. Suggestions have been made in the **review** that might limit or prevent the integration of superfluous **vector** sequences during **transformation** procedures; however, these are not proven and further research is required.

4/3,AB/4 (Item 1 from file: 76)  
DIALOG(R) File 76:Life Sciences Collection  
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02579057 4752520  
Agrobacterium-mediated plant **transformation** with large DNA fragments  
Shibata, D.; Liu, Y. G.  
Kazusa DNA Research Institute, Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Trends in Plant Science vol. 5, no. 8, pp. 354-357 (2000)  
ISSN: 1360-1385  
DOCUMENT TYPE: Journal article; Review article LANGUAGE: ENGLISH  
SUBFILE: Agricultural and Environmental Biotechnology Abstracts

Cosmid **vectors** such as pOCA18 and pLZC3 have been developed that can **transform** plants. However, the low cloning capacity of these **vectors** limits their usefulness. Recently, two research groups have developed **vectors** for the **transformation** of large DNA fragments into plants. These **vectors** are designed to have the characteristics of both bacterial artificial chromosomes (BACs) and binary **vectors** for Agrobacterium-mediated **transformation**. Therefore, large DNA fragments cloned in the T-DNA region can be transferred into a plant genome by Agrobacterium. Indeed, many genomic-DNA fragments (less than or equal to 150 kb) have been introduced successfully into several plant species by these **vectors**. This **transformation** technology has contributed to the map-based cloning (positional cloning) of novel genes defined by mutation from *Arabidopsis*. It should facilitate the isolation of dominant alleles of agronomic importance. Furthermore, the technology will be useful in plant biotechnology, especially for situations that require the simultaneous introduction of several genes, such as those encoding the enzymes of a metabolic pathway.

4/3,AB/5 (Item 1 from file: 94)  
DIALOG(R)File 94:JICST-Eplus  
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05103757 JICST ACCESSION NUMBER: 02AC0335839 FILE SEGMENT: JICST-E  
Laver as a model plant in ocean and genomics.  
MITSUKA OSAMU (1); KITADE YUKIHIRO (2); SAGA NAOTSUNE (2)  
(1) Hokkaido Univ., Graduate School of Fisheries Sci., JPN; (2) Tokai  
Univ., Sch. of Mar. Sci. and Technol.  
Kaiyo to Seibutsu(Aquabiology), 2002, VOL.24,NO.1, PAGE.34-38, FIG.2,  
TAB.1, REF.12  
JOURNAL NUMBER: S0210BAB ISSN NO: 0285-4376  
UNIVERSAL DECIMAL CLASSIFICATION: 639.64 67.082 575.116.4  
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan  
DOCUMENT TYPE: Journal  
ARTICLE TYPE: Commentary  
MEDIA TYPE: Printed Publication  
ABSTRACT: A marine red alga *Porphyra* has recently received great interest  
not only as a valuable marine crop but also as a model plant for  
fundamental and applied studies in marine sciences. *Porphyra* has a  
unique dimorphic life cycle which consists of a leafy gametophytic  
generation and a filamentous sporophytic one. It completes its life  
cycle in laboratory culture within a few months and has a small number  
of chromosomes(2-7) in the haploid phase. The haploid genome sizes in  
the genus *Porphyra*(2.7-5.3\*10<sup>6</sup>bp) are in the same order of magnitude as  
those of *Arabidopsis thaliana*. Genetic analyses, including both  
classical and modern molecular studies are in progress. Now, we are  
performing the following subjects in order to make *Porphyra* a  
sophisticated model organism: cryo-preservation, establishment of  
mutant cell lines, development of host-vector system for  
transformation, *Porphyra* genome project which includes genetic  
map, EST, DNA macro/micro array, etc. We will introduce arrangements  
for an infrastructure of advanced research on *Porphyra* genomics which  
is a key to open the door toward the new marine botany world in this  
review. (author abst.)

4/3,AB/6 (Item 1 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04753069 H.W. WILSON RECORD NUMBER: BGS002003069  
Stamnodes: their morphological and evolutionary significance.  
Fenise Decraene, L. P  
Smets, E. F  
The Botanical Review (Bot Rev) v. 67 no3 (July/Sept. 2001) p. 351-402  
SPECIAL FEATURES: bibl il tab ISSN: 0006-8101  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 20563

4/3,AB/7 (Item 2 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04751956 H.W. WILSON RECORD NUMBER: BGS002001956  
Biology of mammalian L1 retrotransposons.  
Ostertag, Eric M  
Kazazian, Haig H  
Annual Review of Genetics v. 35 (2001) p. 501-38  
SPECIAL FEATURES: bibl il ISSN: 0066-4197  
LANGUAGE: English

COUNTRY OF PUBLICATION: United States  
WORD COUNT: 18786

ABSTRACT: L1 retrotransposons comprise 17% of the human genome. Although most L1s are inactive, some elements remain capable of retrotransposition. L1 elements have a long evolutionary history dating to the beginnings of eukaryotic existence. Although many aspects of their retrotransposition mechanism remain poorly understood, they likely integrate into genomic DNA by a process called target primed reverse transcription. L1s have shaped mammalian genomes through a number of mechanisms. First, they have greatly expanded the genome both by their own retrotransposition and by providing the machinery necessary for the retrotransposition of other mobile elements, such as Alus. Second, they have shuffled non-L1 sequence throughout the genome by a process termed transduction. Third, they have affected gene expression by a number of mechanisms. For instance, they occasionally insert into genes and cause disease both in humans and in mice. L1 elements have proven useful as phylogenetic markers and may find other practical applications in gene discovery following insertional mutagenesis in mice and in the delivery of therapeutic genes. Reprinted by permission of the publisher.

4/3,AB/8 (Item 3 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04504719 H.W. WILSON RECORD NUMBER: BGS01004719  
Recognition and silencing of repeated DNA.

Hsieh, Jenny  
Fire, Andrew  
Annual Review of Genetics v. 34 (2000) p. 187-204

SPECIAL FEATURES: bibl il ISSN: 0066-4197

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 8041

ABSTRACT: Mechanisms for repetition of DNA pose both opportunities and challenges to a functional genome: opportunities for increasing gene expression by amplification of useful sequences, and challenges of controlling amplification by unwanted sequences such as transposons and viruses. Experiments in numerous organisms have suggested the likely existence of a general mechanism for recognition of repeated character in DNA. This **review** focuses (a) on the nature of these recognition mechanisms, and (b) on types of chromatin modification and gene silencing that are used to control repeated DNA. Reprinted by permission of the publisher. Reprinted by permission of the publisher.

4/3,AB/9 (Item 4 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04212907 H.W. WILSON RECORD NUMBER: BGS00022907  
Mercury toxicity in plants.

Patra, Manomita  
Sharma, Archana

The Botanical Review (Bot Rev) v. 66 no3 (July/Sept. 2000) p. 379-422  
SPECIAL FEATURES: bibl il tab ISSN: 0006-8101

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 25426

ABSTRACT: Mercury poisoning has become a problem of current interest as a result of environmental pollution on a global scale. Natural emissions of

mercury form two-thirds of the input; manmade releases form about one-third. Considerable amounts of mercury may be added to agricultural land with sludge, fertilizers, lime, and manures. The most important sources of contaminating agricultural soil have been the use of organic mercurials as a seed-coat dressing to prevent fungal diseases in seeds. In general, the effect of treatment on germination is favorable when recommended dosages are used. Injury to the seed increases in direct proportion to increasing rates of application. The availability of soil mercury to plants is low, and there is a tendency for mercury to accumulate in roots, indicating that the roots serve as a barrier to mercury uptake. Mercury concentration in aboveground parts of plants appears to depend largely on foliar uptake of Hg0 volatilized from the soil. Uptake of mercury has been found to be plant specific in kryophytes, lichens, wetland plants, woody plants, and crop plants. Factors affecting plant uptake include soil or sediment organic content, carbon exchange capacity, oxide and carbonate content, redox potential, formulation used, and total metal content. In general, mercury uptake in plants could be related to pollution level. With lower levels of mercury pollution, the amounts in crops are below the permissible levels. Aquatic plants have shown to be bioaccumulators of mercury. Mercury concentrations in the plants (stems and leaves) are always greater when the metal is introduced in organic form. In freshwater aquatic vascular plants, differences in uptake rate depend on the species of plant, seasonal growth-rate changes, and the metal ion being absorbed. Some of the mercury emitted from the source into the atmosphere is absorbed by plant leaves and migrates to humus through fallen leaves. Mercury-vapor uptake by leaves of the C3 species oats, barley, and wheat is five times greater than that by leaves of the C4 species corn, sorghum, and crabgrass. Such differential uptake by C3 and C4 species is largely attributable to internal resistance to mercury-vapor binding. Airborne mercury thus seems to contribute significantly to the mercury content of crops and thereby to its intake by humans as food. Accumulation, toxicity response, and mercury distribution differ between plants exposed through shoots or through roots, even when internal mercury concentrations in the treated plants are similar. Throughfall and litterfall play a significant role in the cycling and deposition of mercury. The possible causal mechanisms of mercury toxicity are changes in the permeability of the cell membrane, reactions of sulphhydryl (-SH) groups with cations, affinity for reacting with phosphate groups and active groups of ADP or ATP, and replacement of essential ions, mainly major cations. In general, inorganic forms are thought to be more available to plants than are organic ones.

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4 3,AB/10 (Item 5 from file: 98)  
DIALOG(R) File 98:General Sci Abs/Full-Text  
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04265194 H.W. WILSON RECORD NUMBER: BGSA00015194  
LEAFY and the evolution of rosette flowering in violet cress (*Jonopsidium acaule*, Brassicaceae).

Shu, Guoping  
Amaral, Weber; Hileman, Lena C  
American Journal of Botany v. 87 no5 (May 2000) p. 634-41  
SPECIAL FEATURES: bibl 11 ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 5493

ABSTRACT: **Arabidopsis** and most other Brassicaceae produce an elongated inflorescence of mainly ebracteate flowers. However, the early-flowering species violet cress (*Jonopsidium acaule*) and a handful of other species produce flowers singly in the axils of rosette leaves. In **Arabidopsis** the gene LEAFY (LFY) is implicated in both the determination of flower meristem identity and in the suppression of leaves

(bracts) that would otherwise subtend the flowers. In this study we examined the role of LFY homologs in the evolution of rosette flowering in violet cress. We cloned two LFY homologs, *vcLFY1* and *vcLFY2*, from violet cress. Their exon sequences show 90% nucleotide similarity with *Arabidopsis* LFY and 99% similarity to each other. We used *in situ* hybridization to study *vcLFY* expression in violet cress. The patterns were very similar to LFY in *Arabidopsis* except for stronger expression in the shoot apical meristem outside of the region of flower meristem initiation. It is possible that the relatively diffuse expression of *vcLFY* contributes to the lack of bract suppression in violet cress. Additionally, the earliest flowers produced by violet cress express *vcLFY*, suggesting that accelerated flowering in violet cress could also result from changes in the regulation of *vcLFY*. Reprinted by permission of the publisher.

4/3,AB/11 (Item 6 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04264504 H.W. WILSON RECORD NUMBER: BGSAC0014504  
Crown gall disease and *Agrobacterium tumefaciens*: a study of the history, present knowledge, missing information, and impact on molecular genetics.  
Stafford, Helen A  
The Botanical Review (Bot Rev) v. 66 no1 (Jan./Mar. 2000) p. 99-118  
SPECIAL FEATURES: bibl il ISSN: 0006-8101  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 10929

ABSTRACT: The production of crown gall tumors in plants caused by *Agrobacterium tumefaciens* represents a unique disease involving the transfer of DNA from the bacterium to the nucleus of the plant. Vital aspects of this transfer are still being studied. Reprinted by permission of the publisher.

4/3,AB/12 (Item 7 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04255640 H.W. WILSON RECORD NUMBER: BGSAC0005640  
Plant retrotransposons.  
AUGMENTED TITLE: review  
Kumar, Amar  
Bennetzen, Jeffrey L  
Annual Review of Genetics v. 33 (1999) p. 479-532  
SPECIAL FEATURES: bibl il ISSN: 0066-4197  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 22407

ABSTRACT: Retrotransposons are mobile genetic elements that transpose through reverse transcription of an RNA intermediate. Retrotransposons are ubiquitous in plants and play a major role in plant gene and genome evolution. In many cases, retrotransposons comprise over 50% of nuclear DNA content, a situation that can arise in just a few million years. Plant retrotransposons are structurally and functionally similar to the retrotransposons and retroviruses that are found in other eukaryotic organisms. However, there are important differences in the genomic organization of retrotransposons in plants compared to some other eukaryotes, including their often-high copy numbers, their extensively heterogeneous populations, and their chromosomal dispersion patterns. Recent studies are providing valuable insights into the mechanisms involved in regulating the expression and transposition of retrotransposons. This

review describes the structure, genomic organization, expression, regulation, and evolution of retrotransposons, and discusses both their contributions to plant genome evolution and their use as genetic tools in plant biology. Reprinted by permission of the publisher.

4/3,AB/13 (Item 8 from file: 98)  
DIALOG R-File 98:General Sci Abs/Full-Text  
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04255140 H.W. WILSON RECORD NUMBER: EGSA0005140  
Phylogenetic structure in the grass family (Poaceae): evidence from the nuclear gene phytochrome B.

Mathews, Sarah  
Tsai, Focky C; Kellogg, Elizabeth A  
American Journal of Botany v. 87 no1 (Jan. 2000) p. 96-107  
SPECIAL FEATURES: bibl il ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 8359

ABSTRACT: Phylogenetic analyses of partial phytochrome B (PHYB) nuclear DNA sequences provide unambiguous resolution of evolutionary relationships within Poaceae. Analysis of PHYB nucleotides from 51 taxa representing seven traditionally recognized subfamilies clearly distinguishes three early-diverging herbaceous "bambusoid" lineages. First and most basal are Anomochloa and Streptochaeta, second is Pharus, and third is Puelia. The remaining grasses occur in two principal, highly supported clades. The first comprises bambusoid, cryzoid, and pooid genera (the BOP clade); the second comprises panicoid, arundinoid, chloridoid, and centothecoid genera (the PACC clade). The PHYB phylogeny is the first nuclear gene tree to address comprehensively phylogenetic relationships among grasses. It corroborates several inferences made from chloroplast gene trees, including the PACC clade, and the basal position of the herbaceous bamboos Anomochloa, Streptochaeta, and Pharus. However, the clear resolution of the sister group relationship among bambusoids, cryzoids, and pooids in the PHYB tree is novel: the relationship is only weakly supported in ndhF trees and is nonexistent in rbcL and plastid restriction site trees. Nuclear PHYB data support Anomochlooideae, PHaroideae, Pooideae sensu lato, Oryzoideae, Panicoideae, and Chloridoideae, and concur in the polyphyly of both Arundinoideae and Bambusoideae. Reprinted by permission of the publisher.

4/3,AB/14 (Item 9 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04045904 H.W. WILSON RECORD NUMBER: BGSI99045904  
Cellular and molecular biology of the aquaporin water channels.  
Bergnia, Mario  
Nielsen, Soren; Engel, Andreas  
Annual Review of Biochemistry v. 68 (1999) p. 425-58  
SPECIAL FEATURES: bibl il ISSN: 0066-4154  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 12474

ABSTRACT: The high water permeability characteristic of mammalian red cell membranes is now known to be caused by the protein AQP1. This channel freely permits movement of water across the cell membrane, but it is not permeated by other small, uncharged molecules or charged solutes. AQP1 is a tetramer with each subunit containing an aqueous pore likened to an hourglass formed by obversely arranged tandem repeats. Cryoelectron microscopy of reconstituted AQP1 membrane crystals has revealed the

three-dimensional structure at 3-6 Å. AQP1 is distributed in apical and basolateral membranes of renal proximal tubules and descending thin limbs as well as capillary endothelia. Ten mammalian aquaporins have been identified in water-permeable tissues and fall into two groupings. Orthodox aquaporins are water-selective and include AQP2, a vasopressin-regulated water channel in renal collecting duct, in addition to AQP0, AQP4, and AQP5. Multifunctional aquaglyceroporins AQP3, AQP7, and AQP9 are permeated by water, glycerol, and some other solutes. Aquaporins are being defined in numerous other species including amphibia, insects, plants, and microbials. Members of the aquaporin family are implicated in numerous physiological processes as well as the pathophysiology of a wide range of clinical disorders. Reprinted by permission of the publisher.

4/3,AB/15 (Item 10 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04014401 H.W. WILSON RECORD NUMBER: BGSI99014401  
Heat-shock proteins, molecular chaperones, and the stress response:  
evolutionary and ecological physiology.

AUGMENTED TITLE: **review**

Feder, Martin E

Hofmann, Gretchen E

Annual Review of Physiology (Annu Rev Physiol) v. 61 ('99) p. 243-82

SPECIAL FEATURES: bibl 1l ISSN: 0066-4278

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 20648

ABSTRACT: Molecular chaperones, including the heat-shock proteins (Hsps), are a ubiquitous feature of cells in which these proteins cope with stress-induced denaturation of other proteins. Hsps have received the most attention in model organisms undergoing experimental stress in the laboratory, and the function of Hsps at the molecular and cellular level is becoming well understood in this context. A complementary focus is now emerging on the Hsps of both model and nonmodel organisms undergoing stress in nature, on the roles of Hsps in the stress physiology of whole multicellular eukaryotes and the tissues and organs they comprise, and on the ecological and evolutionary correlates of variation in Hsps and the genes that encode them. This focus discloses that (a) expression of Hsps can occur in nature, (b) all species have hsp genes but they vary in the patterns of their expression, (c) Hsp expression can be correlated with resistance to stress, and (d) species' thresholds for Hsp expression are correlated with levels of stress that they naturally undergo. These conclusions are now well established and may require little additional confirmation; many significant questions remain unanswered concerning both the mechanisms of Hsp-mediated stress tolerance at the organismal level and the evolutionary mechanisms that have diversified the hsp genes. With permission, from the Annual **Review** of Physiology, Volume 61, 1999, by Annual **Reviews** Inc. (<http://www.annurev.org> ).

4/3,AB/16 (Item 1 from file: 357)  
DIALOG(R)File 357:Derwent Biotech Res.  
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0242901 DEA Accession No.: 1999-13566

Towards molecular farming in the future: using plant-cell-suspension cultures as bioreactors - for example **vector**-mediated tobacco transgenic plant construction, used for recombinant antibody, protein production, etc. **review**

AUTHOR: Fischer R; Emans N; Schuster F; Hellwig S; Drossard J

CORPORATE AFFILIATE: Tech.Coll.Aachen-Inst.Biol.

Inst. Environ. Chem. Ecotox. Schmalenberg  
CORPORATE SOURCE: Institut fuer Biologie, RWTH Aachen, Worringerweg 1,  
D-52074 Aachen, Germany.  
JOURNAL: Biotechnol. Appl. Biochem. (30, Pt.2, 109-12) 1999  
ISSN: 0885-4513 CODEN: BABIEC  
LANGUAGE: English

ABSTRACT: Plant-suspension cells are **reviewed** as an in vitro system for the production of recombinant protein under carefully controlled certified conditions. Free cell suspensions are considered to be the most suitable for large-scale applications in the biotechnology industry. Plant species used for generation and propagation of suspension cell cultures include **Arabidopsis** sp., **Catharanthus** sp., yew (**Taxus** sp.), rice (**Oryza sativa**), soybean (**Glycine max**), alfalfa (**Medicago sativa**) and tobacco (**Nicotiana tabacum**). Plant cell suspensions can be cultivated in shake flasks or culture vessel using batch, fed-batch, perfusion and continuous culture. For recombinant protein production **Agrobacterium** sp.-mediated **transformation**, microparticle bombardment, electroporation of protoplasts or virus **vectors** can all be used. Tobacco suspension cell cultures have been used to express IgGs, Fab fragments, single chains, bispecific antibody fragments and fusion proteins. Tobacco BY-2 cells have been used for culture using a working volume of 40 l. A 10% (v/v) inoculum with a culture time of 150 hr produced a yield of 7.5 kg fresh cell weight. (52 ref)

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137976	BRASSICA
207558	COTTON
229288	POTATO
38865	SOYA
490457	SUGAR
93591	BEET
50469	SUGAR (W) BEET
490457	SUGAR
52728	CANE
29533	SUGAR (W) CANE
397838	RICE
366124	MAIZE
239324	BARLEY
582106	WHEAT
1717342	TRANSFORM?
742275	VECTOR?
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6282	S5
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S7 69	S6 AND REVIEW?

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8/3,AB/1 (Item 1 from file: 5)  
FILED(R) File 5:Bicsis Previews(R)  
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13164582 BICSIS NO.: 200100371731

Genetic transformation of wheat: Progress during the 1990s into the Millennium.

AUTHOR: Ingram Heidi M; Livesey Nancy L; Power J Brian; Davey Michael R (a)  
AUTHOR ADDRESS: (a)Plant Science Division, School of Biosciences,

University of Nottingham, University Park, Nottingham, NG7 2RD\*\*UK

JOURNAL: Acta Physiologae Plantarum 23 (2):p221-239 2001

MEDIUM: print

ISSN: 0137-5881

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT Wheat transformation technology has progressed

rapidly during the past decade. Initially, procedures developed for protoplast isolation and culture, electroporation- and polyethylene glycol (PEG)-induced DNA transfer enabled foreign genes to be introduced into **wheat** cells. The development of ballistic (microprojectile) bombardment procedures led to a more efficient approach for direct gene transfer. More recently, Agrobacterium-mediated gene delivery procedures, initially developed for the **transformation** of **rice**, have also been used to generate transgenic **wheat** plants. This **review** summarises the considerable progress in **wheat transformation** achieved during the last decade. An increase in food production is essential in order to sustain the increasing world population. This could be achieved by the development of higher yielding varieties with improved nutritional quality and tolerance to biotic and abiotic stresses. Although conventional breeding will continue to play a major role in increasing crop yield, laboratory-based techniques, such as genetic **transformation** to introduce novel genes into crop plants, will be essential in complementing existing breeding technologies. A decade ago, cereals were considered recalcitrant to **transformation**. Since then, a significant research effort has been focused on cereals because of their agronomic status, leading to improved genetic **transformation** procedures (Bommireddi and Jauhar 1997). Initially, the genetic **transformation** of cereals relied on the introduction of DNA into protoplasts and the subsequent production of callus from which fertile plants were regenerated. More recently, major advances have been accomplished in the regeneration of fertile plants from a range of source tissues, providing an essential foundation for the generation of transgenic plants. This **review** summarises procedures, **vectors** and target tissues used for **transformation**, highlights the limitations of current approaches and discusses future trends. The citation of references is limited, where possible, to the most relevant or recent reports.

2001

8/3,AB/2 (Item 2 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
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13059554 BIOSIS NO.: 200100266703  
Transgenesis of *Arabidopsis thaliana* for understanding plant gene structure and functions.  
AUTHOR: Ctndrej Milos (a)  
AUTHOR ADDRESS: (a) Institute of Plant Molecular Biology, Academy of Sciences of the Czech Republic, Branisovska 31, CZ-37005, Ceske Budejovice\*\*Czech Republic  
JOURNAL: Biologia (Bratislava) 56 (1):p1-5 February, 2001  
MEDIUM: print  
ISSN: 0006-3088  
DOCUMENT TYPE: Literature Review  
RECORD TYPE: Abstract  
LANGUAGE: English  
SUMMARY LANGUAGE: English

ABSTRACT: Insertion mutagenesis of *Arabidopsis thaliana* is **reviewed** as efficient means to clone genes known only by phenotype and to correlate gene sequence and function. Random insertions of T-DNA or modified **maize** transposons introduced into *A. thaliana* genome by *Agrobacterium tumefaciens* lead to mutations. The mutation sites are tagged by the T-DNA or modified transposon sequences and they can be cloned by plasmid rescue or iPCR. In order to have 95% probability of hitting all *A. thaliana* genes, 100 000 independent insertion lines should be induced and this number has already been nearly reached. Only minority of insertion mutations are connected with distinct phenotypic effect, but

all insertion mutations in the chosen gene sequence can be selected by pooling insertion lines and utilization of combination of direct and reverse genetic attitudes.

2001

8/3,AB/3 (Item 3 from file: 5)  
DIALOG(R) File 5:Biosis Previews(R)  
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12439958 BIOSIS NO.: 200000239460  
Agrobacterium-mediated **transformation** of cereals: From technique development to its application.

AUTHOR: Nadolska-Orczyk Anna(a); Orczyk Waclaw(a); Przetakiewicz Anna(a)  
AUTHOR ADDRESS: (a)Department of Biotechnology and Cytogenetics, Plant Breeding and Acclimatization Institute, 05-870, Blonie\*\*Poland

JOURNAL: Acta Physiologiae Plantarum 22 (1):p77-88 2000  
ISSN: 0137-5881

DOCUMENT TYPE: Literature Review

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: Agrobacterium tumefaciens is a very useful **vector** to transfer foreign genes into dicotyledonous cells. Monocotyledonous, especially cereals, were considered outside the host range of the bacteria. The main, alternative technique of **transformation** developed for them was delivery of naked DNA (e.g. micro-projectile bombardment, electroporation of protoplasts). The results of Agrobacterium-mediated **transformation** of cereals accumulated during the last few years confirmed that the method was reliable and repeatable also for this group of plants. The most important advantages of Agro-based system include relatively high **transformation** efficiency, integration of defined piece of DNA (transgene) frequently as a single copy, Mendelian transmission to the next generation, simple **transformation** procedure and lower cost of equipment than biolistic. Discussed are the crucial factors of successful Agrobacterium-mediated **transformation** of cereals: type of plant tissue used, A. tumefaciens strains and plasmids (**vectors**), activation of bacterial virulence system and promoter, reporter as well as selectable genes applied for transgene construction. The **review** contains examples of Agrobacterium-based **transformation** methods and practical opportunities of their application as well as the list and description of cereal transgenic plants (**rice, maize, wheat and barley**) obtained after Agrobacterium-mediated **transformation**.

2000

8/3,AB/4 (Item 1 from file: 34)  
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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10298424 Genuine Article#: 505DZ Number of References: 178  
Title: Invited **review**: Use of Ri-mediated **transformation** for production of transgenic plants (ABSTRACT AVAILABLE)

Author(s): Christey MC (REPRINT)

Corporate Source: Crop & Food Res,Private Bag 4704/Christchurch//New Zealand/ (REPRINT); Crop & Food Res,Christchurch//New Zealand/

Journal: IN VITRO CELLULAR & DEVELOPMENTAL BIOLOGY-PLANT, 2001, V37, N6 (NOV-DEC), P687-700

ISSN: 1054-5476 Publication date: 20011100

Publisher: C A B I PUBLISHING, C/O PUBLISHING DIVISION, WALLINGFORD OX10 8DE, CXON, ENGLAND

Language: English Document Type: REVIEW

Abstract: *Agrobacterium rhizogenes*-mediated **transformation** has been used to obtain transgenic plants in 89 different taxa, representing 79 species from 55 genera and 27 families. A diverse range of dicotyledonous plant families is represented, including one Gymnosperm family. In addition to the *Fi* plasmid, over half these plants have been **transformed** with foreign genes, including agronomically useful traits. Plants regenerated from hairy roots often show altered plant morphology such as dwarfing, increased rooting, altered flowering, wrinkled leaves and/or increased branching due to *rol* gene expression. These altered phenotypic features can have potential applications for plant improvement especially in the horticultural industry where such morphological alterations may be desirable. Use of *A. rhizogenes* and *rol* gene **transformation** has tremendous potential for genetic manipulation of plants and has been of particular benefit for improvement of ornamental and woody plants.

8/3,AB/5 (Item 2 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

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09719223 Genuine Article#: 441TU Number of References: 199

Title: Superfluous transgene integration in plants (ABSTRACT AVAILABLE)

Author(s): Smith N (REPRINT); Kilpatrick JB; Whitelam GC

Corporate Source: ADAS Nutr Sci Res Unit, Alcester Rd/Stratford Upon Avon CV37 9RQ//England/ (REPRINT); ADAS Nutr Sci Res Unit, Stratford Upon Avon CV37 9RQ//England/; ADAS Rosemaund, Hereford HR1 3PG//England/; Univ Leicester, Dept Biol, Leicester LE1 7RH, Leics/England/

Journal: CRITICAL REVIEWS IN PLANT SCIENCES, 2001, V20, N3, P215-249

ISSN: 0735-2689 Publication date: 20010000

Publisher: CRC PRESS LLC, 2000 CORPORATE BLVD NW, JOURNALS CUSTOMER SERVICE, BOCA RATON, FL 33431 USA

Language: English Document Type: FVIEW

Abstract: Recent reports suggest the transfer of superfluous DNA sequences to plant genomes during **transformation** processes. This **review** investigates the evidence from the published literature for the prevalence of this phenomenon and highlights methods to limit or prevent DNA transfer and subsequent potentially detrimental evolutionary consequences.

Evidence for superfluous foreign DNA transfer using both *Agrobacterium*-mediated **transformation** and direct DNA transfer methods such as microprojectile bombardment and PEG-mediated **transformation** of protoplasts is reported. In the case of *Agrobacterium*-mediated **transformation**, the lack of information on the integration of sequences from outside of the T-DNA borders has been due to the general belief by researchers that T-DNA processing is precise. This assumption was based on analysis of T-DNA in tumors and as a result the majority of T-DNA integration events have been identified exclusively using DNA probes, which are homologous only to DNA from within the T-DNA borders. Where direct gene transfer protocols are employed, any part of the **transforming** plasmid and indeed accompanying carrier DNA may become integrated into the plant genome. The main body of evidence proving that superfluous **vector** DNA sequences are present in plant genomes **transformed** using direct transfer methods is confined to the identification of plasmid concatamers integrated into plant genomes.

The limited amount of recorded evidence pertaining to superfluous **vector** DNA integration in transgenic plants and **transformed** tissues makes it impossible to draw definitive conclusions as to the

factors involved in promoting this phenomenon. However, there are methods available for removing superfluous sequences from transgenic plants. These have been developed for the removal of selectable marker genes, whose presence in transgenic plants has been a source of much controversy, but can equally be applied to other DNA sequences. Suggestions have been made in the **review** that might limit or prevent the integration of superfluous **vector** sequences during **transformation** procedures; however, these are not proven and further research is required.

8/3,AB/6 (Item 1 from file: 50)  
DIALOG(R) File 50:CAB Abstracts  
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03985377 CAB Accession Number: 20003003941  
Resistance and tolerance to **barley** yellow dwarf in cereals: new perspectives.

Barbieri, R. L.; Oliveira, A. C. de; Carvalho, F. I. F. de  
Departamento de Fitotecnia, Universidade Federal de Pelotas, Caixa  
Postal 354, 96001.970, RS, Brazil.

Journal of New Seeds vol. 2 (2): p.23-35

Publication Year: 2000

ISSN: 1522-886X --

Language: English

Document Type: Journal article

**Barley** yellow dwarf is a cereal virus disease transmitted by aphids. It is an important factor of yield losses for all cereals, including **wheat**, **barley**, oat and triticale. It is caused by related viruses known as BYDVs, members of the Luteoviridae family. Selection for resistance and tolerance to BYDVs is not an easy task to accomplish in breeding programs, because they suffer high environmental influence. In the last years, biotechnology has presented some approaches to complement traditional breeding programmes. These include identification of molecular markers linked to resistance and tolerance genes, in order to make possible marker assisted selection, and **transformation** of hosts with genes conferring resistance to BYDVs.

55 ref.

8/3,AB/7 (Item 2 from file: 50)  
DIALOG(R) File 50:CAB Abstracts  
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03811610 CAB Accession Number: 991612352

**Wheat** starch modification through biotechnology.

Baga, M.; Repellin, A.; Demeke, T.; Caswell, K.; Leung, N.; Abdel-Aal, E. S.; Hucl, P.; Chibbar, R. N.

Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon S7N 0W9, Canada.

Starch/Starke vol. 51 (4): p.111-116

Publication Year: 1999

ISSN: 0038-9056 --

Language: English

Document Type: Journal article

Natural mutations that affect the amylose/amyllopectin ratio in starch are unlikely to develop naturally in **wheat** due to its allohexaploid genome ( $2n = 6x$ ; ABBDD). Biotechnological techniques to modify **wheat** starch are **reviewed**. One of the strategies to modify **wheat** starch structure involves identification of germplasms with null alleles for starch biosynthetic genes, followed by exchange of functional alleles with the identified null alleles through classical plant breeding. This technique has successfully been used to combine the three null alleles for granule bound starch synthase I to develop a

wheat line that produces amylopectin-rich (>95%) starch (waxy starch). Another strategy to alter expression levels of starch biosynthetic genes employs recent advances in molecular biology and genetic engineering of wheat. For this approach, various monocotyledon vectors have been developed that drive expression of wheat starch branching enzyme I (SBEI) cDNA sequences in the anti-sense orientation. Several of the wheat cell lines transformed with the anti-sense vectors express branching enzyme (BE) activity at a significantly lower level than non-transformed cells. One transgenic wheat plant expressing the anti-sense SBEI RNA produces a 10-fold lower level of BE activity in kernels than wild-type wheat. Analysis of starch produced from the transgenic plant shows that starch structure and properties have been altered. 57 ref.

8/3,AB/8 (Item 1 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04935490 H.W. WILSON RECORD NUMBER: BGSA02185490  
Poverty and environmental degradation: challenges within the global economy.  
Makogunje, Akin L  
Environment v. 44 no1 (Jan./Feb. 2002) p. 8-18  
SPECIAL FEATURES: bibl f ill ISSN: 0013-9157  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 7558

ABSTRACT: The challenges of dealing with poverty and environmental degradation within the context of the global economy are discussed. Deepening poverty and environmental degradation are linked, and since the end of the Second World War, the visibility and extent of both of these phenomena has increased. This has occurred in spite of the efforts of the UN and related international agencies to promote global development in a series of well-publicized social and economic development efforts. Globalization is perhaps the single most important development in the world today. Although it exacerbates poverty in some places and among some groups, globalization also has a democratizing potential that may be essential to breaking out of poverty.

8/3,AB/9 (Item 2 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04857477 H.W. WILSON RECORD NUMBER: BGSA02107477  
A waterborne outbreak of Escherichia coli O157:H7 infections and hemolytic uremic syndrome: implications for rural water systems.  
Olsen, Sonja J  
Miller, Gayle; Breuer, Thomas  
Emerging Infectious Diseases (Emerging Infect Dis) v. 8 no4 (Apr. 2002) p. 370-5  
SPECIAL FEATURES: bibl f graph tab ISSN: 1080-6040  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 4577

8/3,AB/10 (Item 3 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04857260 H.W. WILSON RECORD NUMBER: BGSAC2107260  
Role of gravity waves in triggering deep convection during TOGA COARE  
Lac, C  
Lafore, J.-P; Redelsperger, J.-L  
Journal of the Atmospheric Sciences (J Atmos Sci) v. 59 no8 (Apr. 15 2002)  
p. 1293-316  
SPECIAL FEATURES: bibl graph il ISSN: 0022-4928  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 10971

ABSTRACT: The role of gravity waves in the initiation of convection over oceanic regions during the Tropical Ocean Global Atmosphere Coupled Ocean-Atmosphere Response Experiment (TOGA COARE) experiment is investigated. First, an autocorrelation method is applied to infrared temperature observations of convective events from satellite images. It reveals that new deep convective cells often occur a few hours after a previous intense event at a typical distance of a few hundred kilometers. Such fast moving modes (faster than 15 m s<sup>-1</sup>) are interpreted as the trace of gravity waves excited by previous convection and contributing to trigger further convection. Second, the specific case of 11-12 December 1992, during which an active squall line is generated after the collapse of a previous mesoscale convective system (MCS) nearby, is analyzed with a nonhydrostatic model. The triggering of the second MCS is well reproduced explicitly, owing to the use of the two-way interactive grid nesting. The convective source appears to emit pulses of gravity waves on a wide range of small scales. On the contrary, the troposphere response to the convective source exhibits a spectral simplicity. A slowly evolving mode, characterized by an ascent in the PBL and a compensating subsidence in the free troposphere, favors shallow convection and inhibits deep convection, respectively. Traveling modes propagating away from the convective source are characterized by a fast mode ( $\sim$ 50 m s<sup>-1</sup>) and a slower mode ( $\sim$ 25 m s<sup>-1</sup>) associated with the convective and stratiform development of the source, respectively, in agreement with previous studies. A budget analysis reveals the different factors leading to the deep convection triggering. First, an active PBL characterized by strong surface fluxes and mean ascent, initiates shallow convection, lasting about 2 h, inhibited above by the subsiding motions maintaining a dry layer. Second, horizontal advection of moist and cooler air at midlevels, and detrainment from cumuli, contribute to destroy the dry air layer capping the shallow convective layer. Finally, vertical advection induced by the gravity waves passage modulates the vapor and temperature evolution. Ascending phases favor moistening and cooling, whereas subsiding phases stop these effects, delaying the deep convection onset. The triggering occurs after a strong subsidence, when the ascent phases of deep and shallow modes are combined. Reprinted by permission of the publisher.

8-1,AB/11 (Item 4 from file: 98)  
DIALOG.R)File 98:General Sci Abs/Full-Text  
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04663824 H.W. WILSON RECORD NUMBER: BGSAC2103824  
Predicting the risk of Lyme disease: habitat suitability for *Ixodes scapularis* in the north central United States.  
Guerra, Marta  
Walker, Edward; Jones, Carl  
Emerging Infectious Diseases (Emerging Infect Dis) v. 8 no3 (Mar. 2002) p. 269-97

SPECIAL FEATURES: bibl f graph il map tab ISSN: 1080-6040  
LANGUAGE English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 7085

ABSTRACT: The distribution and abundance of *Ixodes scapularis* were studied in Wisconsin, northern Illinois, and portions of the Upper Peninsula of Michigan by inspecting small mammals for ticks and by collecting questing ticks in state parks and natural areas. Environmental data were gathered at a local level (i.e., micro and meso levels), and a geographic information system (GIS) was used with several digitized coverages of environmental data to create a habitat profile for each site and a grid map for Wisconsin and Illinois. Results showed that the presence and abundance of *I. scapularis* varied, even when the host population was adequate. Tick presence was positively associated with deciduous, dry to mesic forests and alfisol-type soils of sandy or loam-sand textures overlying sedimentary rock. Tick absence was associated with grasslands, conifer forests, wet to wet/mesic forests, acidic soils of low fertility and a clay soil texture, and Precambrian bedrock. We performed a discriminant analysis to determine environmental differences between positive and negative tick sites and derived a regression equation to examine the probability of *I. scapularis* presence per grid. Both analyses indicated that soil order and land cover were the dominant contributors to tick presence. We then constructed a risk map indicating suitable habitats within areas where *I. scapularis* is already established. The risk map also shows areas of high probability the tick will become established if introduced. Thus, this risk analysis has both explanatory power and predictive capability. Reprinted by permission of the publisher.

8/3, AB/12 (Item 5 from file: 98)  
DIALOG(R) File 98:General Sci Abs/Full-Text  
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04851481 H.W. WILSON RECORD NUMBER: BGSA02101481  
Ambient air pollution and risk of birth defects in southern California.  
Ritz, Beate  
Yu, Fei; Fruin, Scott  
American Journal of Epidemiology (Am J Epidemiol) v. 155 no1 (Jan. 1 2002)  
p. 17-25  
SPECIAL FEATURES: bibl f tab ISSN: 0002-9262  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 5979

ABSTRACT: The authors evaluated the effect of air pollution on the occurrence of birth defects ascertained by the California Birth Defects Monitoring Program in neonates and fetuses delivered in southern California in 1987-1993. By using measurements from ambient monitoring stations of carbon monoxide (CO), nitrogen dioxide, ozone, and particulate matter <10 mm in aerodynamic diameter, they calculated average monthly exposure estimates for each pregnancy. Conventional, polytomous, and hierarchical logistic regression was used to estimate odds ratios for subgroups of cardiac and orofacial defects. Odds ratios for cardiac ventricular septal defects increased in a dose-response fashion with increasing second-month CO exposure (odds ratio (OR) 2nd quartile CO = 1.62, 95% confidence interval (CI): 1.05, 2.48; OR 3rd quartile CO = 2.09, 95% CI: 1.19, 3.67; OR 4th quartile CO = 2.95, 95% CI: 1.44, 6.05). Similarly, risks for aortic artery and valve defects, pulmonary artery and valve anomalies, and conotruncal defects increased with second-month ozone exposure. The study was inconclusive for other air pollutants. The authors' results are supported by the specificity of the timing of the effect and some evidence from animal data; however, this is the first known study to link ambient air pollution during a vulnerable window of development to human malformations. Confirmation by further studies is needed. Reprinted by permission of the publisher.

8/3, AB/13 (Item 6 from file: 98)

DIALOG(R) File 98:General Sci Abs/Full-Text  
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04756169 H.W. WILSON RECORD NUMBER: BGSA02006169

*Madagasikaria* (Malpighiaceae): a new genus from Madagascar with implications for floral evolution in Malpighiaceae.

Davis, Charles C

American Journal of Botany (Am J Bot) v. 89 no4 (Apr. 2002) p. 699-706

SPECIAL FEATURES: bibl il ISSN: 0002-9122

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 5899

ABSTRACT: *Madagasikaria andersonii* is described here as a new genus and species of Malpighiaceae from Madagascar. The phylogenetic placement of *Madagasikaria* was estimated by using combined data from *ndhF* and *trnL-F* chloroplast sequences and phytochrome (PHYC) and ITS nuclear sequences. It forms a strongly supported clade with the Malagasy endemic genera *Rhynchosphora* and *Microsteira*. Despite nearly identical floral morphology among species in this clade (here called the *madagasikarioid* clade), these genera are easily distinguishable on the basis of their fruits. The schizocarpic fruits of *Madagasikaria* have distinctive mericarps. Each mericarp has a lateral wing, which completely encircles the nut, and a peculiar dorsal wing, which folds over on itself. The morphology of this fruit suggests that the homology of the unusual wing in *Rhynchosphora* is lateral in nature and represents a reduced wing similar to the lateral wing in *Madagasikaria*. Taxa in the *madagasikarioid* clade all appear to be morphologically androdioecious and functionally dioecious, producing both staminate and "bisexual" (i.e., functionally carpellate) individuals. This condition appears to be exceedingly rare in flowering plants and has important implications for floral evolution within Malpighiaceae.

Neotropical Malpighiaceae are pollinated by specialized oil-collecting anthophorine bees of the tribe Centridini and exhibit highly conserved floral morphology despite tremendous diversity in fruit morphology and habit. These oil-collecting bees are absent from the paleotropics, where most members of the Malpighiaceae lack both the oil glands and the typical floral orientation crucial to pollination by neotropical oil-collecting bees. The *madagasikarioids* represent one shift from the neotropical pollination syndrome among Old World Malpighiaceae. Reprinted by permission of the publisher.

8/3,AB/14 (Item 7 from file: 98)

DIALOG(R) File 98:General Sci Abs/Full-Text  
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04754361 H.W. WILSON RECORD NUMBER: BGSA02004361

The use of DNA sequencing (ITS and *trnL-F*), AFLP, and fluorescent in situ hybridization to study allotetraploid *Miscanthus* (Poaceae).

Hodkinson, Trevor R

Hase, Mark W; Takahashi, Chigusa

American Journal of Botany (Am J Bot) v. 89 no2 (Feb. 2002) p. 279-86

SPECIAL FEATURES: bibl il ISSN: 0002-9122

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 6937

ABSTRACT. Two clones of *Miscanthus*, grown under the names *M. Xgiganteus* and *M. sacchariflorus*, have been used in biomass trials in Europe, but neither the identity of these clones nor their origin has been established. DNA sequencing, amplified fragment length polymorphism (AFLP), and chromosome studies confirm that *M. Xgiganteus* is an allotetraploid ( $2n = 3x = 57$ ) combining genomes from *M. sinensis* ( $2n = 2x = 38$ ) and *M. sacchariflorus* ( $2n = 38$  or 76). Two alleles of the internal transcribed spacer of 18S-25S

nuclear ribosomal DNA (ITS) were discovered in polymerase chain reaction products of *M. Xgiganteus*. Cloning of these revealed that one matched *M. sinensis* and the other *M. sacchariflours*. Plastid *trnL* intron and *trnL-F* spacer sequences showed that the maternal lineage of *M. Xgiganteus* was *M. sacchariflours*. Fluorescent in situ hybridization, FISH, was used to investigate genome organization in *Miscanthus* but was unable to differentiate between the different parental genomes present in *M. Xgiganteus*, indicating that two parental genomes are still extremely similar at the repetitive DNA level. This study is an example in which rDNA sequences and AFLP fingerprints permit identification of the parental genomes in a hybrid, but FISH methods, at the repetitive DNA level (including genomic in situ hybridization, GISH), were unable to do so because their sequences remain too similar. Reprinted by permission of the publisher.

3.3,AB/15 (Item 8 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04761939 H.W. WILSON RECORD NUMBER: BGS02001939  
Hypoviruses and chestnut blight: exploiting viruses to understand and modulate fungal pathogenesis.

Dawe, Angus L  
Nuss, Donald L  
Annual Review of Genetics v. 35 (2001) p. 1-29  
SPECIAL FEATURES: bibl il ISSN: 0066-4197  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 13672

ABSTRACT: Fungal viruses are considered unconventional because they lack an extracellular route of infection and persistently infect their hosts, often in the absence of apparent symptoms. Because mycoviruses are limited to intracellular modes of transmission, they can be considered as intrinsic fungal genetic elements. Such long-term genetic interactions, even involving apparently asymptomatic mycoviruses, are likely to have an impact on fungal ecology and evolution. One of the clearest examples supporting this view is the phenomenon of hypovirulence (virulence attenuation) observed for strains of the chestnut blight fungus, *Cryphonectria parasitica*, harboring members of the virus family Hypoviridae. The goal of this chapter is to document recent advances in hypovirus molecular genetics and to provide examples of how that progress is leading to the identification of virus-encoded determinants responsible for altering fungal host phenotype, insights into essential and dispensable elements of hypovirus replication, revelations concerning the role of G-protein signaling in fungal pathogenesis, and new avenues for enhancing biological control potential. Reprinted by permission of the publisher.

3.3,AB/16 (Item 9 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04760973 H.W. WILSON RECORD NUMBER: BGS02000973  
Applied evolution.  
Bull, J. J  
Wichman, H. A  
Annual Review of Ecology and Systematics v. 32 (2001) p. 183-217  
SPECIAL FEATURES: bibl graph il tab ISSN: 0066-4162  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 16986

ABSTRACT Evolutionary biology is widely perceived as a discipline with relevance that lies purely in academia. Until recently, that perception was largely true, except for the often neglected role of evolutionary biology in the improvement of agricultural crops and animals. In the past two decades, however, evolutionary biology has assumed a broad relevance extending far outside its original bounds. Phylogenetics, the study of Darwin's theory of "descent with modification," is now the foundation of disease tracking and of the identification of species in medical, pharmacological, or conservation settings. It further underlies bioinformatics approaches to the analysis of genomes. Darwin's "evolution by natural selection" is being used in many contexts, from the design of biotechnology protocols to create new drugs and industrial enzymes, to the avoidance of resistant pests and microbes, to the development of new computer technologies. These examples present opportunities for education of the public and for nontraditional career paths in evolutionary biology. They also provide new research material for people trained in classical approaches. Reprinted by permission of the publisher.

8/3,AB/17 (Item 10 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04750782 H.W. WILSON RECORD NUMBER: BGSAC02000782  
The role of breeding system and inbreeding depression in the maintenance of an outcrossing mating strategy in *Silene virginica* (Caryophyllaceae).  
Dudash, Michele R  
Fenster, Charles B  
American Journal of Botany (Am J Bot) v. 88 no.11 (Nov. 2001) p. 1953-9  
SPECIAL FEATURES: kibl il ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 7471

ABSTRACT: The goal of this study was to understand the interaction among breeding system, mating system, and expression of inbreeding depression in the nectaraghriditic, primarily hummingbird-pollinated, iteroparous, short-lived perennial *Silene virginica*. We performed hand-selfed and hand-outcrossed pollinations in the field, conducted detailed floral observations within individual flowers and plants, and assayed adult tissue from flowering plants for a genetic estimate of population outcrossing rate. We quantified the opportunity for geitonogamy as the proportion of days each plant exhibited simultaneous male and female function, i.e., asynchronous expression of male- and female-phased flowers. Expression of cumulative inbreeding depression based on germination rate and total flower production in the glasshouse was (similar) 40% and was congruent with the estimated high outcrossing rate of 0.89. Floral observations demonstrated strong temporal protandry within each flower (diandromy) as well as complete spatial separation between male and female function within each flower (herkogamy). On average, 29% of the time there were both male- and female-phased flowers present on an individual plant. We conclude that our estimate of inbreeding depression is compatible with a largely outcrossing mating system and the amount of selfing observed, likely results from geitonogamy. This study illustrates the utility of examining both the causes and the consequences of inbreeding via selfing to provide additional insights into the evolution of plant mating systems. Reprinted by permission of the publisher.

8/3,AB/18 (Item 11 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04669024 H.W. WILSON RECORD NUMBER: BGSAC01169024

Traveling toxics: the science, policy, and management of persistent organic pollutants.  
Eckley, Noelle  
Environment v. 43 no7 (Sept. 2001) p. 24-36  
SPECIAL FEATURES: bibl fil map tab ISSN: 0013-9157  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 7573

ABSTRACT: International agreements have sought to address the problems caused by the release of persistent organic pollutants (POPs). POPs are organic chemicals characterized by their persistence in the environment, tendency to accumulate in the food chain, and ability to travel long distances in air and water, posing risks to human health and the environment far from the site of their release. Though most countries have banned these chemicals, international action to address POPs does not merely codify the status quo. The signing of the Stockholm Convention, which includes several specific measures to regulate 12 POPs, on May 23, 2001, is a notable example of such action. Indeed, the biggest upcoming policy challenge is the ratification and implementation of the convention; it will enter force only after 50 countries ratify it. Other international activities on chemicals are ongoing, and some address similar substances.

8'3,AB/19 (Item 12 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04657154 H.W. WILSON RECORD NUMBER: BGS01157154  
Wavelet analysis of simulated tropical convective clouds systems. Part II: decomposition of convective-scale and mesoscale structure.  
Yanai, Jun-Ichi  
Moncrieff, Mitchell W; Wu, Xiaoqing  
Journal of the Atmospheric Sciences (J Atmos Sci) v. 58 no8 (Apr. 15 2001)  
p. 868-76  
SPECIAL FEATURES: bibl graph il ISSN: 0022-4928  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 5207

ABSTRACT: Numerically simulated three-dimensional tropical convective systems were analyzed using a wavelet approach in which the vertical shear of the ambient wind is used as a decomposition criterion. The method objectively decomposes the simulated systems into their two primary components, namely organized deep convection and a mesoscale stratiform region. This reproduces the standard model of highly organized mesoscale convective systems as well as giving an objective characterization of less organized regimes. It demonstrates the vertical component of wind shear as a statistically useful criterion in addition to its better known role as a quasideterministic mechanism controlling the organization of convection and its scale selection. Reprinted by permission of the publisher.

8'3,AB/20 (Item 13 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04518101 H.W. WILSON RECORD NUMBER: BGS01018121  
Transgenic insecticidal corn: the agronomic and ecological rationale for its use.  
Ortman, Eldon E  
Barry, B. Dean; Buschman, Lawrence L  
BioScience (BioScience) v. 51 no11 (Nov. 2001) p. 900-6  
SPECIAL FEATURES: bibl ISSN: 0006-3568

LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 5700

8/3,AB/21 (Item 14 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04517240 H.W. WILSON RECORD NUMBER: BGSA01017240  
FLUXNET: a new tool to study the temporal and spatial variability of  
ecosystem-scale carbon dioxide, water vapor, and energy flux densities.

Baldocchi, Dennis

Falge, Eva; Gu, Lianhong

Bulletin of the American Meteorological Society (Bull Am Meteorol Soc) v.  
82 no11 (Nov. 2001) p. 2415-34

SPECIAL FEATURES: bibl il map ISSN: 0003-0007

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 13202

ABSTRACT: FLUXNET is a global network of micrometeorological flux measurement sites that measure the exchanges of carbon dioxide, water vapor, and energy between the biosphere and atmosphere. At present over 140 sites are operating on a long-term and continuous basis. Vegetation under study includes temperate conifer and broadleaved (deciduous and evergreen) forests, tropical and boreal forests, crops, grasslands, chaparral, wetlands, and tundra. Sites exist on five continents and their latitudinal distribution ranges from 70{degree}N to 30{degree}S. FLUXNET has several primary functions. First, it provides infrastructure for compiling, archiving, and distributing carbon, water, and energy flux measurement, and meteorological, plant, and soil data to the science community. (Data and site information are available online at the FLUXNET Web site, <http://www-eosdis.ornl.gov/FLUXNET/>.) Second, the project supports calibration and flux intercomparison activities. This activity ensures that data from the regional networks are intercomparable. And third, FLUXNET supports the synthesis, discussion, and communication of ideas and data by supporting project scientists, workshops, and visiting scientists. The overarching goal is to provide information for validating computations of net primary productivity, evaporation, and energy absorption that are being generated by sensors mounted on the NASA Terra satellite. Data being compiled by FLUXNET are being used to quantify and compare magnitudes and dynamics of annual ecosystem carbon and water balances, to quantify the response of stand-scale carbon dioxide and water vapor flux densities to controlling biotic and abiotic factors, and to validate a hierarchy of soil-plant-atmosphere trace gas exchange models. Findings so far include 1) net CO<sub>2</sub> exchange of temperate broadleaved forests increases by about 5.7 g C m<sup>-2</sup> day<sup>-1</sup> for each additional day that the growing season is extended; 2) the sensitivity of net ecosystem CO<sub>2</sub> exchange to sunlight doubles if the sky is cloudy rather than clear; 3) the spectrum of CO<sub>2</sub> flux density exhibits peaks at timescales of days, weeks, and years, and a spectral gap exists at the month timescale; 4) the optimal temperature of net CO<sub>2</sub> exchange varies with mean summer temperature; and 5) stand age affects carbon dioxide and water vapor flux densities. Reprinted by permission of the publisher.

8/3,AB/22 (Item 15 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04517138 H.W. WILSON RECORD NUMBER: BGSA01017138  
Granule-bound starch synthase (GBSSI) gene phylogeny of wild tomatoes  
(*Solanum* L. section *Lycopersicon* (Mill.) Wettst. subsection

Lycopersicon).

Peralta, Iris E

Spooner, David M

American Journal of Botany (Am J Bot) v. 88 no10 (Oct. 2001) p. 1888-902

SPECIAL FEATURES: bibl il map ISSN: 0022-9122

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 10197

**ABSTRACT:** Eight wild tomato species are native to western South America and one to the Galapagos Islands. Different classifications of tomatoes have been based on morphological or biological criteria. Our primary goal was to examine the phylogenetic relationships of all nine wild tomato species and closely related outgroups, with a concentration on the most widespread and variable tomato species *Solanum peruvianum*, using DNA sequences of the structural gene granule-bound starch synthase (GESS1, or waxy). Results show some concordance with previous morphology-based classifications and new relationships. The ingroup comprised a basal polytomy composed of the self-incompatible green-fruited species *S. chilense* and the central to southern Peruvian populations of *S. peruvianum*, *S. habrochaites*, and *S. pennellii*. A derived clade contains the northern Peruvian populations of *S. peruvianum* (also self-incompatible, green-fruited), *S. chmielewskii*, and *S. neocrickii* (self-compatible, green-fruited), and the self-compatible and red- to orange- to yellow-fruited species *S. cheesmaniae*, *S. lycopersicum*, and *S. pimpinellifolium*. Outgroup relationships are largely concordant with prior chloroplast DNA restriction site phylogenies, support *S. juglandifolium* and *S. ochranthum* as the closest outgroup to tomatoes with *S. lycopersicoides* and *S. sitiens* as basal to these, and support allogamy, self-incompatibility, and green fruits as primitive in the tomato clade.  
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14515431 H.W. WILSON RECORD NUMBER: BGSAC1015431

Functional significance of variation in bryophyte canopy structure.

Rice, Steven K

Collins, David; Anderson, Ann M

American Journal of Botany (Am J Bot) v. 88 no9 (Sept. 2001) p. 1568-76

SPECIAL FEATURES: bibl il ISSN: 0022-9122

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 8968

**ABSTRACT:** In most bryophytes, the thickness of boundary layers (i.e., unstirred layers) that surrounds plant surfaces governs rates of water loss. Architectural features of canopies that influence boundary layer thickness affect the water balance of bryophytes. Using field samples (9.3 cm diameter cushions) from 12 populations (11 species) of mosses and liverworts, we evaluated the relationship between canopy structure and boundary layer properties. Canopy structure was characterized using a contact surface probe to measure canopy depth along perpendicular transects at spatial scales ranging from 0.3 to 30 mm on 186 points per sample. Semivariance in depth measurements at different spatial scales was used to estimate three architectural properties: surface roughness ( $L_r$ ), the scale of roughness elements ( $S_r$ ), and fine scale surface texture, the latter characterized by the fractal dimension ( $D$ ) of the canopy profile. Boundary layer properties were assessed by evaporation of ethanol from samples in a wind tunnel at wind speeds from 0.6 to 4.2 m s<sup>-1</sup> and applied to characterize mass transfer using principles of dynamic similarity (i.e., using dimensionless representations of conductance and flow). In addition,

particle image velocimetry (PIV) was used to visualize and quantify flow over two species. All cushions exhibited the characteristics of turbulent as opposed to laminar boundary layers, and conductance increased with surface roughness. Bryophyte canopies with higher Lr had greater conductances at all wind speeds. Particle image velocimetry analysis verified that roughness elements interacted with flow and caused turbulent eddies to enter canopies, enhancing evaporation. All three morphological features were significantly associated with evaporation. When Lr, Sr, and D were incorporated with a flow parameter into a conductance model using multiple linear regression, the model accounted for 91% of the variation in mass transfer. Reprinted by permission of the publisher.

5/3,AB/24 (Item 17 from file: 98)  
DIALOG(F)File 98:General Sci Abs/Full-Text  
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04514582 H.W. WILSON RECORD NUMBER: BGSA01014582  
The distribution of estuarine and oceanic water masses on the southern shore of O'ahu, Hawai'i: ecological and coastal management implications, and novel methodology.

Ed Parnell, P  
Limnology and Oceanography (Limnol Oceanogr) v. 46 no6 (Sept. 2001) p. 1468-85

SPECIAL FEATURES: bibl il map ISSN: 0024-3590

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 11054

ABSTRACT: The distribution of estuarine and oceanic water masses along the shelf of Mamala Bay, O'ahu, Hawaii, were determined by use of larval supply and recruitment patterns of benthic invertebrate species, stable C and N isotopic compositions of the suspension-feeding bivalve, *Spondylus tenebrosus*, turbidity, drifter, and CTD data. The recruitment of different species among estuaries was used to associate larval species with particular estuarine waters. Recruitment patterns of these species along the shelf were then used to infer water-mass distributions along the shelf. The spatial recruitment pattern of an oceanic lepadomorph barnacle, *Conchoecetes virgatum*, was useful to infer shelf areas exposed to oceanic waters. Water-mass distributions inferred from the recruitment distribution of these species concurred with spatial patterns of turbidity and stable C and N isotopic compositions of *S. tenebrosus*, as well as drifter observations. Water-mass distributions observed in this study also concurred with biological distributional patterns observed in other studies, such as distributions of phytoplankton and zooplankton and the distribution of coral bio-erosion in the Bay. The ecological implications of this work include further evidence of the physical control of recruitment and biological pattern and the possible control of patch dynamics on the scale of kilometers due to significant recruitment variability at this scale. The prevailing distribution of water masses determined in this study also has important implications for the management of watersheds associated with Mamala Bay. Reprinted by permission of the publisher.

5/3,AB/25 (Item 18 from file: 98)  
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04511678 H.W. WILSON RECORD NUMBER: BGSA01011678  
Implications of mating patterns for conservation of the endangered plant *Eriogonum ovalifolium* var. *wineum* (Polygonaceae).  
Neel, Malle C  
Ross Ibarra, Jeffrey; Ellstrand, Norman C

American Journal of Botany (Am J Bot) v. 88 no7 (July 2001) p. 1214-22

SPECIAL FEATURES: bibl il map ISSN: 0002-9122

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 9139

**ABSTRACT:** Mating patterns have direct application to conservation because of their influence on structuring genetic diversity within and among populations and on maintaining that diversity over time. We measured population and family outcrossing rates, biparental inbreeding, correlation of outcrossed paternity, and inbreeding coefficients in six populations from throughout the ecological range of the endangered plant *Eriogonum ovalifolium* var. *vineum* using naturally pollinated families. The taxon was primarily outcrossed: population outcrossing rates averaged 0.80 (SE 0.03) and family outcrossing rates averaged 0.88 (SE 0.03); neither rate varied among populations. Five population rates were significantly different from 1 while family rates differed from 1 in only one population. We found high correlated outcrossed paternity and evidence for biparental inbreeding in five populations each. As expected from the predominantly outcrossed mating system, levels of diversity were high and inbreeding coefficients among maternal individuals were low (averaging -0.05, SE 0.12). Differences between inbreeding coefficients of progeny (average 0.21, SE 0.06) and mothers indicated selection against homozygous offspring. These results indicate that it is important to maintain large populations to prevent increases in inbreeding and to maintain pollinator communities to facilitate outcrossing. Reprinted by permission of the publisher.

8/3/AB/26 (Item 19 from file: 98)

DIALOG(R) File 98:General Sci Abs/Full-Text

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04509718 H.W. WILSON RECORD NUMBER: BGSA01009718

Transition-matrix model of bicturbation and radionuclide diagenesis.

Shull, David H

Limnology and Oceanography (Limnol Oceanogr) v. 46 no4 (June 2001) p. 905-16

SPECIAL FEATURES: bibl il ISSN: 0024-3590

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 9689

**ABSTRACT:** Bicturbation rates in muddy sediments are thought to be due primarily to the reworking activities of benthic deposit feeders. However, current mathematical models of bicturbation do not explicitly link rates of particle mixing with realistic biological reworking mechanisms. To address this problem, I present a transition-matrix model of bioturbation that quantitatively links the reworking activities of individual organisms and community-level particle-mixing rates. Solutions to the model are presented for two kinds of tracers; particle-reactive radionuclides with a constant input flux and conservative tracers added to the sediment as a pulse. The model was used to predict the vertical profiles of excess  $^{234}\text{Th}$  and  $^{210}\text{Pb}$  in the field. The model parameters were determined from benthic community-structure data. Model predictions were then compared to measured profiles of these tracers. On the basis of this comparison, I inferred that maldanid polychaetes at the study site were collecting sediment at the sediment-water interface and depositing it at depth. This transport mechanism had a large effect on the predicted tracer profiles. A sensitivity analysis of the model indicated that deposit feeding by the two most abundant species, *Mediomastus ambiseta* and *Nucula annulata*, was the most important process determining the burial rate of the tracers. The model results also indicated that the combined effects of deposit feeding and sedimentation were sufficient to determine the vertical distributions of excess  $^{234}\text{Th}$  and  $^{210}\text{Pb}$  at the study site. Reprinted by permission of the

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8/3,AB/27 (Item 20 from file: 98)  
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04509214 H.W. WILSON RECORD NUMBER: B3SA01009214  
Size-dependent sex allocation within flowers of the annual herb *Clarkia unguiculata* (Onagraceae): ontogenetic and among-plant variation.  
Mazer, Susan J  
Lawson, Kelly Ann  
American Journal of Botany (Am J Bot) v. 88 no5 (May 2001) p. 819-31  
SPECIAL FEATURES: bibl il ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 11248

**ABSTRACT:** The relative allocation of resources to male and female functions may vary among flowers within and among individual plants for many reasons. Several theoretical models of sex allocation in plants predict a positive correlation between the resource status of a flower or individual and the proportion of reproductive resources allocated to female function. These models assume that, independent of resource status, a negative correlation exists between male and female investment. Focusing on the allocation of resources within flowers, we tested these theoretical predictions and this assumption using the annual *Clarkia unguiculata* (Onagraceae). We also sought preliminary evidence for a genetic component to these relationships. From 116 greenhouse-cultivated plants representing 30 field-collected maternal families, multiple flowers and fruits per plant were sampled for gamete production, pollen: ovule ratio, seed number, ovule abortion, seed biomass/fruit, mean individual seed mass, and petal area. If sex allocation changes as predicted, then (1) assuming that flowers produced early have access to more resources than those produced later, basal flowers should exhibit a higher absolute and proportional investment in female function than distal flowers and (2) plants of high resource status (large plants) should produce flowers with a higher proportional investment in female function than those of low resource status. Within plants, variation in floral traits conformed to the first prediction. Among plants and families, no significant effects of plant size (dry stem biomass) on intrafloral proportional sex allocation were observed. We detected no evidence for a negative genetic correlation between male and female investment per flower, even when controlling for plant size.  
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04508278 H.W. WILSON RECORD NUMBER: B3SA01008278  
The evolutionary ecology of nut dispersal.  
Vander Wall, Stephen B  
The Botanical Review (Bot Rev) v. 67 no1 Jan./Mar. 2001 p. 74-117  
SPECIAL FEATURES: bibl tab ISSN: 0006-8101  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 27955

**ABSTRACT:** A variety of nut producing plants have mutualistic seed-dispersal interactions with animals (rodents and corvids) that scatter-hoard their nuts in the soil. The goals of this **review** are to summarize the widespread horticultural, botanical, and ecological literature pertaining to nut dispersal in *Juglans*, *Carya*, *Quercus*, *Fagus*,

Castanæ, Castanopsis, Lithocarpus, Corylus, Aesculus, and Prunus; to examine the evolutionary histories of these mutualistic interactions; and to identify the traits of nut-bearing plants and nut-dispersing rodents and jays that influence the success of the mutualism. These interactions appear to have originated as early as the Paleocene, about 60 million years ago. Most nuts appear to have evolved from ancestors with wind-dispersed seeds, but the ancestral form of dispersal in almonds (*Prunus spp.*) was by frugivorous animals that ingested fruit. Nut-producing species have evolved a number of traits that facilitate nut dispersal by certain rodents and corvids while serving to exclude other animals that act as parasites of the mutualism. Nuts are nutritious food sources, often with high levels of lipids or proteins and a caloric value ranging from 5.7 to 153.5 kJ per propagule, 10-1000 times greater than most wind-dispersed seeds. These traits make nuts highly attractive food items for dispersers and nut predators. The course of nut development tends to reduce losses of nuts to insects, microbes, and nondispersing animals, but despite these measures predispersal and postdispersal nut mortality is generally high. Chemical defenses (e.g., tannins) in the cotyledons or the husk surrounding the nut discourage some nut predators. Masting of nuts (periodic, synchronous production of large nut crops) appears to reduce losses to insects and to increase the number of nuts dispersed by animals, and it may increase cross-pollination. Scatter hoarding by rodents and corvids removes nuts from other sources of nut predation, moves nuts away from source trees where density-dependent mortality is high (sometimes to habitats or microhabitats that favor seedling establishment), and buries nuts in the soil (which reduces rates of predation and helps to maintain nut viability). The large nutrient reserves of nuts not only attract animal dispersers but also permit seedlings to establish a large photosynthetic surface or extensive root system, making them especially competitive in low-light environments (e.g., deciduous forest) and semi-arid environments (e.g., dry mountains, Mediterranean climates). The most important postestablishment causes of seedling failure are drought, insufficient light, browsing by vertebrate herbivores, and competition with forbs and grasses. Because of the nutritional qualities of nuts and the synchronous production of large nut crops by a species throughout a region, nut trees can have pervasive impacts on other members of ecological communities. Nut-bearing trees have undergone dramatic changes in distribution during the last 16,000 years, following the glacial retreat from northern North America and Europe, and the current dispersers of nuts (i.e., squirrels, jays, and their relatives) appear to have been responsible for these movements. Reprinted by permission of the publisher.

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04506267 H.W. WILSON RECORD NUMBER: BGS01006267  
Patterns of leaf-pathogen infection in the understory of a Mexican rain forest: incidence, spatiotemporal variation, and mechanisms of infection.  
Garcia-Guzman, Graciela  
Dirzo, Rodolfo  
American Journal of Botany (Am J Bot. v. 88 no4 (Apr. 2001) p. 634-45  
SPECIAL FEATURES: bibl 11 ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 7646

ABSTRACT: This study assessed the levels of damage by leaf pathogens and their variability in terms of host species, space (four mature forest sites) and season of the year (dry and rainy), and the mechanisms of infection in the understory of the Los Tuxtlas tropical rain forest. Sixty-five percent of the species surveyed in the dry season (N: 49) and 64.9% of those surveyed in the rainy season (N = 57) were damaged by fungi.

Leaf area damaged per plant, on average, was <1% (range: 0.25-20.52%). There was considerable variation in the degree of infection among species, but not among sites and seasons. The survey showed that 43% of the leaves were damaged by herbivores and pathogens concurrently, 16% showed damage by insect herbivory alone, and only 1.4% of the sampled leaves showed damage by pathogens alone. Pathogenicity assays experimentally confirmed that the predominant mechanism of fungal establishment was wounding, such as that caused by herbivory (or other similar sources), and only rarely did infection occur through direct contact (without wounds). The results revealed the omnipresence of leaf fungal infection, although with low damage per plant, and the importance of herbivores in the facilitation of fungal infection in tropical understory plants. Reprinted by permission of the publisher.

8/3,AB/30 (Item 23 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04506264 H.W. WILSON RECORD NUMBER: BGSA01006264  
Effects of virus infection and light environment on population dynamics of *Eupatorium makinoi* (Asteraceae).  
Funayama, Sachiko  
Terashima, Ichiro; Yahara, Tetsukazu  
American Journal of Botany (Am J Bot: v. 88 no4 (Apr. 2001) p. 616-22  
SPECIAL FEATURES: bibl il ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 4730

ABSTRACT: We studied the effects of virus infection on dynamics of three *Eupatorium makinoi* populations in contrasting light environments, Gora-dani (a shaded population) and Minou 1 and Minou 2 (open-site populations). Censuses of the plants were taken for 8 yr in Gora-dani and 4 yr in Minou 1 and Minou 2. After the epidemics of virus infection, most plants were virus infected at both sites. The number of plants and the proportion of flowering individuals decreased rapidly and simultaneously in the shaded population in Gora-dani. By contrast, in the open-site populations of Minou, the proportion of flowering plants decreased first, and then the number of plants decreased gradually. Growth analysis of the plants in the Gora-dani population revealed that stem growth was significantly suppressed by infection and that flowering and survivorship of the infected plants decreased with reducing plant height. Since light availability affected plant growth and thereby flowering and survivorship, the differences in population dynamics between the two field sites could be caused by the differences in light environments. Although populations in open sites may persist for considerable periods after virus epidemics, the individual local populations of *E. makinoi* would eventually become extinct irrespective of light environments. Reprinted by permission of the publisher.

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04504733 H.W. WILSON RECORD NUMBER: BGSA01004733  
Molecular-functional studies of adaptive genetic variation in prokaryotes and eukaryotes.  
Watt, Ward B  
Dean, Antony M  
Annual Review of Genetics v. 34 (2000) p. 593-622  
SPECIAL FEATURES: bibl il ISSN: 0066-4197  
LANGUAGE: English

COUNTRY OF PUBLICATION: United States  
WORD COUNT: 13410

ABSTRACT: Knowledge of both prokaryotic and eukaryotic organisms is essential to the study of molecular evolution. Their common ancestry mandates that their molecular functions share many aspects of adaptation and constraint, yet their differences in size, ploidy, and structural complexity also give rise to divergent evolutionary options. We explore the interplay of adaptation, constraint, and neutrality in their evolution by the use of genetic variants to probe molecular function in context of molecular structure, metabolic organization, and phenotype-environment interactions. Case studies ranging from bacteria to butterflies, flies, and vertebrates emphasize, among other points: (a) the importance of moving from initial recording of evolutionary pattern variation to studying the processes underlying the patterns, by experiment, reconstructive inference, or both; (b) the complementarity, not conflict, of finding different performance and fitness impacts of natural variants in prokaryotes or eukaryotes, depending on the nature and magnitude of the variants, their locations and roles in pathways, the nature of molecular function affected, and the resulting organismal phenotype-environment interactions leading to selection or its absence; (c) the importance of adaptive functional interaction of different kinds of variants, as in gene expression variants versus variants altering polypeptide properties, or interaction of changes in enzymes' active sites with complementary changes elsewhere that adjust catalytic function in different ways, or coadaptation of different steps' properties in pathways; (d) the power afforded by combining structural and functional analyses of variants with study of the variants' phenotype-environment interactions to understand how molecular changes affect (or fail to affect) adaptive mechanisms "in the wild." Comparative study of prokaryotes and eukaryotes in this multifaceted way promises to deliver both new insights into evolution and a host of Reprinted by permission of the publisher. Reprinted by permission of the publisher.

8/3/AB/32 (Item 25 from file: 98:  
DIALOG-R File 98:General Sci Abs/Full-Text  
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04503815 H.W. WILSON RECORD NUMBER: BGSA01003815  
Mechanisms of differential pollen donor performance in wild radish,  
*Raphanus sativus* (Brassicaceae).  
Marshall, Diane L  
Diggle, Pamela K  
American Journal of Botany (Am J Bot) v. 88 no2 (Feb. 2001) p. 242-57  
SPECIAL FEATURES: bibl 11 ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 13592

ABSTRACT: In order to understand the characters on which sexual selection might operate in plants, it is critical to assess the mechanisms by which pollen competition and mate choice occur. To address this issue we measured a number of postpollination characters, ranging from pollen germination and pollen tube growth to final seed paternity, in wild radish. Crosses were performed using four pollen donors on a total of 16 maternal plants (four each from four families). Maternal plants were grown under two watering treatments to evaluate the effects of maternal tissue on the process of mating. The four pollen donors differed significantly in number of seeds sired and differed overall in the mating characters measured. However, it was difficult to associate particular mechanistic characters with ability to sire seeds, perhaps because of interactions among pollen donors within styles or among pollen donors and maternal plants. The process of pollen tube growth and fertilization differed substantially among maternal watering treatments, with many early events occurring more quickly in

stressed plants. Seed paternity, however, was somewhat more even among pollen donors used on stressed maternal plants, suggesting that when maternal tissue is more competent, mating is slowed and is more selective. Reprinted by permission of the publisher.

8/3,AB/33 (Item 26 from file: 98)  
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04502916 H.W. WILSON RECORD NUMBER: BGSA01002916  
Trans-Atlantic dispersal and phylogeograph of *Cerastium arcticum*  
(Caryophyllaceae) inferred from RAPD and SCAR markers.

Hagen, Aslaug R  
Giese, Henriette; Brochmann, Christian  
American Journal of Botany (Am J Bot) v. 88 no1 (Jan. 2001) p. 103-12  
SPECIAL FEATURES: bibl graph map tab ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 8055

ABSTRACT: *Cerastium arcticum* is an autogamous pioneer species with a distribution limited to the North Atlantic region. It has been suggested that such species must have survived in ice-free refugia on both sides of the Atlantic throughout the last, or even several, of the Pleistocene glaciations, because they lack special adaptations for long-distance dispersal. To address the possibility for recent trans-Atlantic dispersal of *C. arcticum*, we analyzed random amplified polymorphic DNA (RAPD) and sequence characterized amplified region (SCAR) differentiation among 26 populations of this high-polyplloid species. Three SCAR markers were obtained that verified the main patterns identified in the RAPD analysis. Eighty-four multilocus RAPD phenotypes were observed in the 126 plants analyzed, based on 35 polymorphic markers. Multivariate analyses and analyses of molecular variance (AMOVAs) identified two highly divergent groups of populations: one arctic group (western and eastern Greenland, and the archipelagos of Svalbard and Franz Josef Land) and one nonarctic group (southern and northern Norway, and Iceland), indicating that *C. arcticum* is composed of two lineages with different evolutionary histories. However, there was little geographic structuring within each lineage, in spite of the fact that both lineages are disjunctly distributed across the Atlantic. Occurrence of very similar, in some cases even identical RAPD multilocus phenotypes on both sides of the Atlantic in this autogamous allopolyploid is most probably caused by postglacial dispersal. The present geographic distribution of *C. arcticum* may thus have been established after trans-Atlantic expansion from two Weichselian refugia, one for each evolutionary lineage. Unexpectedly, the level of intrapopulational variation increased towards the north. This may reflect that interpopulational migration is most extensive in the treeless arctic environment, where the species has a more continuous distribution than in the more southerly areas. Reprinted by permission of the publisher.

8/3,AB/34 (Item 27 from file: 98)  
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04563394 H.W. WILSON RECORD NUMBER: BGSA00133994  
Perspectives on American mathematics.  
Hunger Parshall, Karen  
Bulletin of the American Mathematical Society (Bull Am Math Soc) v. 37 no4  
Oct. 2000 p. 381-405  
SPECIAL FEATURES: bibl ISSN: 0273-0979  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States

WORD COUNT: 14902

ABSTRACT: A research-level community of mathematicians developed in the United States in the closing quarter of the nineteenth century. Since that time, American mathematicians have regularly paused to assess the state of their community and to reflect on its mathematical output. This paper analyzes a series of such reflections!Beginning with Simon Newcomb's thoughts on the state of the exact sciences in America in 1874 and culminating with the 1988 commentaries on the 100 problems of mathematics!DD discussed at Princeton's bicentennial celebrations in 1946!Aagainst a backdrop of broader historical trends. Reprinted by permission of the publisher. Reprinted by permission of the publisher.

8/3.AE/35 (Item 28 from file: 98)  
DIALOG(R) File 98:General Sci Abs/Full-Text  
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04382840 H.W. WILSON RECORD NUMBER: BGSA00132840  
An investigation of ice production mechanisms in small cumuliform clouds using a 3D model with explicit microphysics. Part I: model description.  
Cvitchinnikov, Mikhail  
Foggin, Yefim L  
Journal of the Atmospheric Sciences (J Atmos Sci) v. 57 no18 (Sept. 15 2000) p. 2989-3003  
SPECIAL FEATURES: bibl il ISSN: 0022-4928  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 12019

ABSTRACT: A new cloud model that combines a three-dimensional nonhydrostatic dynamical framework with explicit liquid- and ice-phase microphysics and a detailed treatment of ice nucleation and multiplication processes is presented. The use of 28 size bins to describe each cloud drop and ice particle spectra allows the authors to account for all major microphysical processes. A detailed scavenging model has been implemented to calculate the collection rate of contact ice nuclei by cloud drops. In addition to contact nucleation, the model accounts for deposition, condensation-freezing, and immersion ice nucleation mechanisms, as well as for secondary ice production via rime splintering. The model performance is illustrated by a simulation of a New Mexican cumulus cloud. Combination of high 100-m spatial resolution with a new initialization procedure that promotes development of small eddies results in a cloud with a more realistic distribution of liquid water content compared to simulations initialized by the standard IDdbubble!DD approach. Reprinted by permission of the publisher. Reprinted by permission of the publisher.

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04381155 H.W. WILSON RECORD NUMBER: BGSA00131155  
Biotechnology and our food supply.  
McKey, Maureen A  
Santerre, Charles R  
Nutrition Today (Nutr Today) v. 35 no4 (July/Aug. 2000) p. 120-8  
SPECIAL FEATURES: bibl il ISSN: 0029-666X  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 6834

ABSTRACT: Biotechnology and its agricultural applications are discussed. The following topics are covered: the definition of biotechnology,

biotechnology techniques, global experience with genetically improved crops, increased world food supplies, reduced need for chemical pesticides, environmentally friendly crops, safety assessment and regulation of food from genetically modified plants, and enhanced nutritional content, quality, and taste in engineered foods.

8-3,AB '37 (Item 30 from file: 98)  
DIALOG(F)File 98:General Sci Abs/Full-Text  
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04380022 H.W. WILSON RECORD NUMBER: BGSA00130222  
Sensitivity of tropical west Pacific oceanic squall lines to tropospheric wind and moisture profiles.

Lucas, Christopher  
Zipser, Edward J; Ferrier, Brad S  
Journal of the Atmospheric Sciences (J Atmos Sci) v. 57 no15 (Aug. 1 2000)  
p. 2351-73  
SPECIAL FEATURES: bibl 11 ISSN: 0022-4928  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 13564

ABSTRACT: Two-dimensional experiments using the Goddard Cumulus Ensemble model are performed in order to examine the influence of environmental profiles of wind and humidity on the dynamical and microphysical structure of mesoscale convective systems (MCSs) over the tropical oceans. The initial environments used in this study are derived from the results of a cluster analysis of the TOGA COARE sounding data. The model data are analyzed with methods and measurements similar to those used in observational studies. Experiments to test the sensitivity of MCSs to the thermodynamic profile focus on the role of humidity in the free troposphere. In the experiments, a constant amount of relative humidity is added to every level above the boundary layer. As humidity is increased, model storms transition from weak, unsteady systems with little precipitation to strong, upshear-tilted systems with copious rainfall. This behavior is hypothesized to be the result of the entrainment of environmental air into the updraft cores. Experiments to test the sensitivity of MCSs to the kinematic profile focus on the amount of vertical wind shear in the midlevels, between approximately 2 and 10 km. Five kinematic profiles are used. The dynamical and microphysical characteristics of the runs changed dramatically in different shear environments. Shear in the midlevels affects the convective systems by altering the perturbation pressure field. Stronger shear results in a broader and deeper mesolow below the updraft and a more intense dynamic high above the leading edge. Reprinted by permission of the publisher.  
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04363957 H.W. WILSON RECORD NUMBER: BGSA00115352  
Court in the act.  
Mendelson, Joseph  
The Ecologist v. 30 no3 (May 2000) p. 48-9  
ISSN: 0013-1311  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United Kingdom  
WORD COUNT: 2142

ABSTRACT: The Center for Food Safety has filed a lawsuit against the FDA over its premarket safety-testing and labeling policy on genetically

modified (GM) food. The legal action, filed in the U.S. District Court of Columbia on May 27, 1998, was taken in response to the FDA's deregulation of genetically engineered foods in 1992 on the basis that GM foods present no different risks than do traditional foods. The Center for Food Safety lawsuit seeks to mandate the FDA to treat all genetic modifications to food produced by genetic engineering methods as food additives, to carry out a comprehensive environmental review of all GM foods made commercially available, and to ensure the labeling of all GM foods.

8/3/AB/39 (Item 32 from file: 93)  
DIALOG(R) File 93:General Sci Abs/Full-Text  
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04273994 H.W. WILSON RECORD NUMBER: BGSA00023994  
Interim report on genomics of *Escherichia coli*.

Piley, M  
Serres, M. H  
Annual Review of Microbiology v. 54 (2000) p. 341-411  
SPECIAL FEATURES: bibl tab ISSN: 0066-4227  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 2563

ABSTRACT. We present a summary of recent progress in understanding *Escherichia coli* K-12 gene and protein functions. New information has come both from classical biological experimentation and from using the analytical tools of functional genomics. The content of the *E. coli* genome can clearly be seen to contain elements acquired by horizontal transfer. Nevertheless, there is probably a large, stable core of >3500 genes that are shared among all *E. coli* strains. The gene-enzyme relationship is examined, and, in many cases, it exhibits complexity beyond a simple one-to-one relationship. Also, the *E. coli* genome can now be seen to contain many multiple enzymes that carry out the same or closely similar reactions. Some are similar in sequence and may share common ancestry; some are not. We discuss the concept of a minimal genome as being variable among organisms and obligatorily linked to their life styles and defined environmental conditions. We also address classification of functions of gene products and avenues of insight into the history of protein evolution.  
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8/3/AB/40 (Item 33 from file: 93)  
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04273907 H.W. WILSON RECORD NUMBER: BGSA00023907

Mercury toxicity in plants.

Patra, Manomita  
Sharma, Archana  
The Botanical Review (Bot Rev) v. 66 no3 (July/Sept. 2000) p. 379-422  
SPECIAL FEATURES: bibl tab ISSN: 0006-8101  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 25426

ABSTRACT. Mercury poisoning has become a problem of current interest as a result of environmental pollution on a global scale. Natural emissions of mercury form two-thirds of the input; manmade releases form about one third. Considerable amounts of mercury may be added to agricultural land with sludge, fertilizers, lime, and manures. The most important sources of contaminating agricultural soil have been the use of organic mercurials as a seed-coat dressing to prevent fungal diseases in seeds. In general, the effect of treatment on germination is favorable when

recommended dosages are used. Injury to the seed increases in direct proportion to increasing rates of application. The availability of soil mercury to plants is low, and there is a tendency for mercury to accumulate in roots, indicating that the roots serve as a barrier to mercury uptake. Mercury concentration in aboveground parts of plants appears to depend largely on foliar uptake of Hg0 volatilized from the soil. Uptake of mercury has been found to be plant specific in bryophytes, lichens, wetland plants, woody plants, and crop plants. Factors affecting plant uptake include soil or sediment organic content, carbon exchange capacity, oxide and carbonate content, redox potential, formulation used, and total metal content. In general, mercury uptake in plants could be related to pollution level. With lower levels of mercury pollution, the amounts in crops are below the permissible levels. Aquatic plants have shown to be bioaccumulators of mercury. Mercury concentrations in the plants (stems and leaves) are always greater when the metal is introduced in organic form. In freshwater aquatic vascular plants, differences in uptake rate depend on the species of plant, seasonal growth-rate changes, and the metal ion being absorbed. Some of the mercury emitted from the source into the atmosphere is absorbed by plant leaves and migrates to humus through fallen leaves. Mercury-vapor uptake by leaves of the C3 species oats, **barley**, and **wheat** is five times greater than that by leaves of the C4 species corn, sorghum, and crabgrass. Such differential uptake by C3 and C4 species is largely attributable to internal resistance to mercury-vapor binding. Airborne mercury thus seems to contribute significantly to the mercury content of crops and thereby to its intake by humans as food. Accumulation, toxicity response, and mercury distribution differ between plants exposed through shoots or through roots, even when internal mercury concentrations in the treated plants are similar. Throughfall and litterfall play a significant role in the cycling and deposition of mercury. The possible causal mechanisms of mercury toxicity are changes in the permeability of the cell membrane, reactions of sulphhydryl (-SH) groups with cations, affinity for reacting with phosphate groups and active groups of ADP or ATP, and replacement of essential ions, mainly major cations. In general, inorganic forms are thought to be more available to plants than are organic ones. Reprinted by permission of the publisher.

S/3,AB/41 (Item 34 from file: 98)  
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04272503 H.W. WILSON RECORD NUMBER: EGSA00022503  
Synthesis of native proteins by chemical ligation.  
Dawson, Philip E  
Kent, Stephen B. H  
Annual Review of Biochemistry v. 69 (2000) p. 923-60  
SPECIAL FEATURES: bibl il ISSN: 0066-4154  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 12238

ABSTRACT: In just a few short years, the chemical ligation of unprotected peptide segments in aqueous solution has established itself as the most practical method for the total synthesis of native proteins. A wide range of proteins has been prepared. These synthetic molecules have led to the elucidation of gene function, to the discovery of novel biology, and to the determination of new three-dimensional protein structures by both NMR and X-ray crystallography. The facile access to novel analogs provided by chemical protein synthesis has led to original insights into the molecular basis of protein function in a number of systems. Chemical protein synthesis has also enabled the systematic development of proteins with enhanced potency and specificity as candidate therapeutic agents. Reprinted by permission of the publisher.

8/3/AB/42 (Item 35 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04272490 H.W. WILSON RECORD NUMBER: BGS00022490  
Protein splicing and related forms of protein autoprocessing.  
Paulus, Henry  
Annual Review of Biochemistry v. 69 (2000) p. 447-96  
SPECIAL FEATURES: bibl il ISSN: 0066-4154  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 18571

ABSTRACT: Protein splicing is a form of posttranslational processing that consists of the excision of an intervening polypeptide sequence, the intein, from a protein, accompanied by the concomitant joining of the flanking polypeptide sequences, the exteins, by a peptide bond. It requires neither cofactors nor auxiliary enzymes and involves a series of four intramolecular reactions, the first three of which occur at a single catalytic center of the intein. Protein splicing can be modulated by mutation and converted to highly specific self-cleavage and protein ligation reactions that are useful protein engineering tools. Some of the reactions characteristic of protein splicing also occur in other forms of protein autoprocessing, ranging from peptide bond cleavage to conjugation with nonprotein moieties. These mechanistic similarities may be the result of convergent evolution, but in at least one case--hedgehog protein autoprocessing--there is definitely a close evolutionary relationship to protein splicing. Reprinted by permission of the publisher.

8/3/AE/43 (Item 36 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04267707 H.W. WILSON RECORD NUMBER: BGS00017707  
Factors affecting establishment of a gypsophyte: the case of *Lepidium subulatum* (Brassicaceae).  
Escudero, Adrian  
Iriondo, Jose M; Olano, Jose M  
American Journal of Botany (Am J Bot) v. 87 nof (June 2000) p. 861-71  
SPECIAL FEATURES: bibl il ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 10321

ABSTRACT: The restriction of vascular plants to gypsum-rich soils under arid or semiarid climates has been reported by many authors in different parts of the world. However, factors controlling the presence of gypsophytes on these soils are far from understood. We investigated the establishment of *Lepidium subulatum*, a gypsophyte, in a nondisturbed semiarid gypsum-soil landscape in central Spain, both from spatial and temporal perspectives. Over 1400 seedlings were tagged, and their growth and survival were monitored for a 2-yr period. Several biotic and abiotic variables were measured to determine the factors controlling the emergence and early survival. These variables included the cover of annual plants, bryophytes, lichens, litter, gypsum crystals, bare fraction and cover of each perennial plant, and several soil properties (gravel, fine gravel, and fine-earth fraction, conductivity, pH, gypsum content, organic matter and penetrometer soil resistance). Our results support the linkage of gypsophily with some physical properties of the surface crust. Seedlings tended to establish on the gypsum surface crust, and their survival was size dependent, probably as a consequence of the necessity of rooting below the surface crust before summer drought arrives. However, once seedlings

emerged, a higher survival rate occurred on the alluvial soils of the piedmont-slope boundary where soil crusts are absent or thinner. We conclude that *Lepidium subulatum* may be considered a refuge model endemic with a distribution range that occupies a reduced fraction of a wider habitat from which it is probably excluded by competition. Reprinted by permission of the publisher.

8/3,AB/44 (Item 37 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04065194 H.W. WILSON RECORD NUMBER: BGSA00015194  
LEAFY and the evolution of rosette flowering in violet cress (*Jonapsidium acaule*, Brassicaceae).

Shu, Guoping  
Amaral, Weber; Hileman, Lena C  
American Journal of Botany v. 87 no5 (May 2000) p. 634-41  
SPECIAL FEATURES: bibl il ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 5493

ABSTRACT: *Arabidopsis* and most other *Brassicaceae* produce an elongated inflorescence of mainly ebracteate flowers. However, the early-flowering species violet cress (*Jonapsidium acaule*) and a handful of other species produce flowers singly in the axils of rosette leaves. In *Arabidopsis* the gene *LEAFY* (*LFY*) is implicated in both the determination of flower meristem identity and in the suppression of leaves (bracts) that would otherwise subtend the flowers. In this study we examined the role of *LFY* homologs in the evolution of rosette flowering in violet cress. We cloned two *LFY* homologs, *vcLFY1* and *vcLFY2*, from violet cress. Their exon sequences show 89% nucleotide similarity with *Arabidopsis LFY* and 99% similarity to each other. We used *in situ* hybridization to study *vcLFY* expression in violet cress. The patterns were very similar to *LFY* in *Arabidopsis* except for stronger expression in the shoot apical meristem outside of the region of flower meristem initiation. It is possible that the relatively diffuse expression of *vcLFY* contributes to the lack of bract suppression in violet cress. Additionally, the earliest flowers produced by violet cress express *vcLFY*, suggesting that accelerated flowering in violet cress could also result from changes in the regulation of *vcLFY*. Reprinted by permission of the publisher.

8/3,AB/45 (Item 38 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04064504 H.W. WILSON RECORD NUMBER: BGSA00014504  
Crown gall disease and *Agrobacterium tumefaciens*: a study of the history, present knowledge, missing information, and impact on molecular genetics.

Stafford, Helen A  
The Botanical Review (Bot Rev) v. 66 no1 (Jan./Mar. 2000) p. 99-118  
SPECIAL FEATURES: bibl il ISSN: 0006-8101  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 10929

ABSTRACT: The production of crown gall tumors in plants caused by *Agrobacterium tumefaciens* represents a unique disease involving the transfer of DNA from the bacterium to the nucleus of the plant. Vital aspects of this transfer are still being studied. Reprinted by permission of the publisher.

8/3,AB/46 (Item 39 from file: 98)  
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04264428 H.W. WILSON RECORD NUMBER: BGSA00014428  
Phylogeny of the Bangiophycidae (Rhodophyta) and the secondary  
endosymbiotic origin of algal plastids.  
Oliveira, Mariana C  
Bhattacharya, Debashish  
American Journal of Botany (Am J Bot) v. 87 no4 (Apr. 2000) p. 482-92  
SPECIAL FEATURES: bibl il ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 8143

ABSTRACT: The Rhodophyta (red algae) are composed of the subclasses Bangiophycidae and Florideophycidae. Two evolutionarily interesting features of the Bangiophycidae are: (1) they are the ancestral pool from which the more morphologically complex taxa in the Florideophycidae have arisen and (2) they are the sources of the plastids, through secondary endosymbioses, for the Cryptophyta, Haptophyta, and the Heterokonta. To understand Bangiophycidae phylogeny and to gain further insights into red algal secondary endosymbioses, we sequenced the plastid-encoded small subunit ribosomal DNA (rDNA) coding region from nine members of this subclass and from two members of the Florideophycidae. These sequences were included in phylogenetic analyses with all available red algal plus chlorophyll a + c algal plastid rDNA coding regions. Our results are consistent with a monophyletic origin of the Florideophycidae with these taxa forming a sister group of the Bangiales. The Bangiophycidae is of a paraphyletic origin with orders such as the Porphyridiales polyphyletic and distributed over three independent red algal lineages. The plastids of the heterokonts are most closely related to members of the Cyanidium-Galdieria group of Porphyridiales and are not directly related to cryptophyte and haptophyte plastids. The phylogenies provide strong evidence for the independent origins of these "complex" algal plastids from different members of the Bangiophycidae. Reprinted by permission of the publisher.

8/3,AE-47 (Item 40 from file: 98)  
DIALOG+E)File 98:General Sci Abs/Full-Text  
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04259241 H.W. WILSON RECORD NUMBER: BGSA00009241  
Gene mapping in the 20th and 21st centuries: statistical methods, data  
analysis, and experimental design.  
Terwilliger, Joseph D  
Goring, Harald H. H  
Human Biology (Hum Biol) v. 72 no1 (Feb. 2000) p. 63-132  
SPECIAL FEATURES: bibl il ISSN: 0018-7143  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 31712

ABSTRACT: Part of a special section on anthropological genetics in the 21st century. The theory and practice of gene mapping at the end of the 20th century are reviewed. Most methods of linkage and linkage disequilibrium analysis are shown to be similar fundamentally, with differences between them being related more to study design and ascertainment than to technical details of the underlying statistical analysis. A new focus in the field of statistical genetics is proposed that highlights more clearly the primacy of study design as the means to increase power for gene mapping.

8/3,AB '48 (Item 41 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04256371 H.W. WILSON RECORD NUMBER: BGS00006372  
Perspective: the pace of modern life: measuring rates of contemporary  
microevolution.

Hendry, Andrew P

Kinnison, Michael T

Evolution (Evolution) v. 53 no6 (Dec. 1999) p. 1637-53

SPECIAL FEATURES: bibl il ISSN: 0014-3820

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 14481

ABSTRACT: We evaluate methods for measuring and specifying rates of microevolution in the wild, with particular regard to studies of contemporary, often deemed "rapid," evolution. A considerable amount of ambiguity and inconsistency persists within the field, and we provide a number of suggestions that should improve study design, inference, and clarity of presentation. (1) Some studies measure change over time within a population (allochronic) and others measure the difference between two populations that had a common ancestor in the past (synchronous). Allochronic studies can be used to estimate rates of "evolution," whereas synchronous studies more appropriately estimate rates of "divergence." Rates of divergence may range from a small fraction to many times the actual evolutionary rates in the component populations. (2) Some studies measure change using individuals captured from the wild, whereas others measure differences after rearing in a common environment. The first type of study can be used to specify "phenotypic" rates and the later "genetic" rates. (3) The most commonly used evolutionary rate metric, the darwin, has a number of theoretical shortcomings. Studies of microevolution would benefit from specifying rates in standard deviations per generation, the haldane. (4) Evolutionary rates are typically specified without an indication of their precision. Readily available methods for specifying confidence intervals and statistical significance (regression, bootstrapping, randomization) should be implemented. (5) Microevolutionists should strive to accumulate time series, which can reveal temporal shifts in the rate of evolution and can be used to identify evolutionary patterns. (6) Evolutionary rates provide a convenient way to compare the tempo of evolution across studies, traits, taxa, and time scales, but such comparisons are subject to varying degrees of confidence. Comparisons across different time scales are particularly tenuous. (7) A number of multivariate rate measures exist, but considerable theoretical development is required before their utility can be determined. We encourage the continued investigation of evolutionary rates because the information they provide is relevant to a wide range of theoretical and practical issues.

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8/3,AB 49 (Item 42 from file: 98)  
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04255540 H.W. WILSON RECORD NUMBER: BGS00005640  
Plant retrotransposons.

AUGMENTED TITLE: review

Humar, Amar

Henetzen, Jeffrey L

Annual Review of Genetics v. 33 (1999) p. 479-532

SPECIAL FEATURES: bibl il ISSN: 0066-4197

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

COUNTRY OF PUBLICATION: United States  
WORD COUNT: 8359

ABSTRACT: Phylogenetic analyses of partial phytochrome B (PHYB) nuclear DNA sequences provide unambiguous resolution of evolutionary relationships within Poaceae. Analysis of PHYB nucleotides from 51 taxa representing seven traditionally recognized subfamilies clearly distinguishes three early-diverging herbaceous "bambusoid" lineages. First and most basal are *Anomochloa* and *Streptochaeta*, second is *Pharus*, and third is *Puelia*. The remaining grasses occur in two principal, highly supported clades. The first comprises bambusoid, oryzoid, and pooid genera (the BOP clade); the second comprises panicoid, arundinoid, chloridoid, and centothecoid genera (the PACC clade). The PHYB phylogeny is the first nuclear gene tree to address comprehensively phylogenetic relationships among grasses. It corroborates several inferences made from chloroplast gene trees, including the PACC clade, and the basal position of the herbaceous bamboos *Anomochloa*, *Streptochaeta*, and *Pharus*. However, the clear resolution of the sister group relationship among bambusoids, oryzoids, and pooids in the PHYB tree is novel: the relationship is only weakly supported in *ndhF* trees and is nonexistent in *rbcL* and plastid restriction site trees. Nuclear PHYB data support *Anomochloideae*, *Pharoideae*, *Pocideae* sensu lato, *Oryzoideae*, *Panicoideae*, and *Chloridoideae*, and concur in the polyphyly of both *Arundinoideae* and *Bambusoideae*. Reprinted by permission of the publisher.

8/3/AB/52 (Item 45 from file: 98)  
DIALOG(F) File 98:General Sci Abs/Full-Text  
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04050531 H.W. WILSON RECORD NUMBER: BGSA99050531  
Chloroplast DNA evidence for the evolution of *Microseris* (Asteraceae) in Australia and New Zealand after long-distance dispersal from western North America.

Vijverberg, Kitty  
Mes, Ted H. M; Bachmann, Konrad  
American Journal of Botany v. 86 no10 (Oct. 1999) p. 1448-63  
SPECIAL FEATURES: bibl il map ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 10164

ABSTRACT: Restriction site mutations and *trnL(UAA)-trnF(GAA)* intergenic spacer length variants in the chloroplast genome were used to investigate the phylogenetic relationships among 53 Australian and New Zealand *Microseris* populations and to assess their position within their primarily North American genus. The study was performed to enhance understanding of evolutionary processes within this unique example of intercontinental dispersal and subsequent adaptive radiation. A southern blot method using four-base restriction enzymes and fragment separation on polyacrylamide gels resulted in 55 mutations of which 30 were potentially phylogenetically informative. Most mutations were small indels of <162 bp, 80% of which were <21 bp. The small indels were useful for phylogenetic reconstruction of Australasian *Microseris* as judged by the high consistency indexes. The results confirmed the monophyly of the Australian and New Zealand *Microseris*. The occurrence of "hard" basal polytomies in the most parsimonious trees indicated that rapid radiation has occurred early in the history of the taxon. The monophyly of *M. lanceolata*, which includes the self-incompatible ecotypes of the Australian mainland, was confirmed. Within this species three clades were found that reflect more geographic distribution than morphological entities, suggesting that migration and possibly introgression between different ecotypes, or parallel evolution of similar adaptations, has occurred. One of the three clades was supported by a 162-bp deletion in the *trnL-trnF* spacer, while a subgroup of this exhibited also a tandemly repeated *trnF* exon. The data were inconclusive.

about the monophyly of the second Australasian species, *M. scapigera*, which comprises the New Zealand, Tasmanian, and autofertile ecotypes of Australia. Reprinted by permission of the publisher.

8/3,AB/53 (Item 46 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04050513 H.W. WILSON RECORD NUMBER: BGSA99050513  
Bacterial biocatalysts: molecular biology, three-dimensional structures, and biotechnological applications of lipases.

AUGMENTED TITLE: **review**

Jaeger, K-E

Dijkstra, B. W; Reetz, M. T

Annual Review of Microbiology v. 53 (1999) p. 315-51

SPECIAL FEATURES: bibl il ISSN: 0066-4227

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 14938

ABSTRACT: Bacteria produce and secrete lipases, which can catalyze both the hydrolysis and the synthesis of long-chain acylglycerols. These reactions usually proceed with high regioselectivity and enantioselectivity, and, therefore, lipases have become very important stereoselective biocatalysts used in organic chemistry. High-level production of these biocatalysts requires the understanding of the mechanisms underlying gene expression, folding, and secretion. Transcription of lipase genes may be regulated by quorum sensing and two-component systems; secretion can proceed either via the Sec-dependent general secretory pathway or via ABC transporters. In addition, some lipases need folding catalysts such as the lipase-specific foldases and disulfide-bond-forming proteins to achieve a secretion-competent conformation. Three-dimensional structures of bacterial lipases were solved to understand the catalytic mechanism of lipase reactions. Structural characteristics include an a/b hydrolase fold, a catalytic triad consisting of a nucleophilic serine located in a highly conserved Gly-X-Ser-X-Gly pentapeptide, and an aspartate or glutamate residue that is hydrogen bonded to a histidine. Four substrate binding pockets were identified for triglycerides: an oxyanion hole and three pockets accommodating the fatty acids bound at positions sn-1, sn-2, and sn-3. The differences in size and the hydrophilicity/hydrophobicity of these pockets determine the enantioselectivity of a lipase. The understanding of structure-function relationships will enable researchers to tailor new lipases for biotechnological applications. At the same time, directed evolution in combination with appropriate screening systems will be used extensively as a novel approach to develop lipases with high stability and enantioselectivity. Reprinted by permission of the publisher.

8/3,AB/54 (Item 47 from file: 98)  
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04045904 H.W. WILSON RECORD NUMBER: BGSI99045904  
Cellular and molecular biology of the aquaporin water channels.  
Bergna, Mario

Nielsen, Soren; Engel, Andreas

Annual Review of Biochemistry v. 68 (1999) p. 425-58

SPECIAL FEATURES: bibl il ISSN: 0066-4154

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 12474

ABSTRACT: The high water permeability characteristic of mammalian red cell membranes is now known to be caused by the protein AQP1. This channel freely permits movement of water across the cell membrane, but it is not permeated by other small, uncharged molecules or charged solutes. AQP1 is a tetramer with each subunit containing an aqueous pore likened to an hourglass formed by obversely arranged tandem repeats. Cryoelectron microscopy of reconstituted AQP1 membrane crystals has revealed the three-dimensional structure at 3-6 Å. AQP1 is distributed in apical and basolateral membranes of renal proximal tubules and descending thin limbs as well as capillary endothelia. Ten mammalian aquaporins have been identified in water-permeable tissues and fall into two groupings. Orthodox aquaporins are water-selective and include AQP1, a vasopressin-regulated water channel in renal collecting duct, in addition to AQP0, AQP4, and AQP5. Multifunctional aquaglyceroporins AQP3, AQP7, and AQP9 are permeated by water, glycerol, and some other solutes. Aquaporins are being defined in numerous other species including amphiabia, insects, plants, and microbials. Members of the aquaporin family are implicated in numerous physiological processes as well as the pathophysiology of a wide range of clinical disorders. Reprinted by permission of the publisher.

8/3,AB/55 (Item 48 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04042080 H.W. WILSON RECORD NUMBER: BGSA99042080  
Genetic relationships between parasite virulence and transmission in the rodent malaria *Plasmodium chabaudi*.  
Mackinnon, Margaret J  
Read, Andrew F  
Evolution (Evolution) v. 53 no3 (June 1999) p. 689-703  
SPECIAL FEATURES: bibl 1l ISSN: 0014-3820  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 10646

ABSTRACT: Genetic relationships between virulence and transmission in the rodent malaria parasite *Plasmodium chabaudi* were investigated. Two assumptions of the parasite-centered trade-off model of the evolution of virulence--that higher replication rates lead to higher levels of virulence and to higher levels of transmission--were tested using inbred laboratory mice infected with *P. chabaudi*. The virulence and transmission of 8 parasite clones isolated from the wild were measured, and the across-clone genetic relationships between replication rate, virulence, and transmission were examined. Results supported the validity of both assumptions.

8/3,AB/56 (Item 49 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04038175 H.W. WILSON RECORD NUMBER: BGSI99038175  
Blood pressure: genetic and environmental influences.  
Gerrer, Linda M  
Halperstein, Robert A  
Human Biology (Hum Biol) v. 71 no4 (Aug. 1999) p. 467-73  
SPECIAL FEATURES: bibl 1l ISSN: 0018-7143  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 106936

ABSTRACT: An introduction to a special issue on blood pressure and its genetic and environmental influences. Some of the specific aspects related to blood pressure variation are addressed in this issue. The aim of the

issue is to help bring together a vast and ever growing body of research and reveal areas for future research. The history of blood pressure research is outlined, and a brief description of each of the 9 papers in the issue is given.

8/3,AB/57 (Item 50 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04036555 H.W. WILSON RECORD NUMBER: BGSAA99036555  
Wind pollination and reproductive assurance in *Linanthus parviflorus* (Polemoniaceae), a self-incompatible annual.

Goodwillie, Carol  
American Journal of Botany (Am J Bot) v. 86 no7 (July 1999) p. 948-54  
SPECIAL FEATURES: bibl il ISSN: 0002-9122  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 6437

ABSTRACT: Wind pollination was experimentally demonstrated in *Linanthus parviflorus* (Polemoniaceae), a predominantly beefly-pollinated, self-incompatible annual. Seed set in plants enclosed in mesh tents that excluded pollinators but allowed airborne pollen flow provided evidence for wind pollination, and the extent of seed set due to wind pollination was compared to that in open-pollinated controls and pollen-supplemented treatments. Additional controls were included to test for possible confounding effects of the mesh tent. Mean seed number in open-pollinated plants was 72.8-81.1% of that in pollen-supplemented plants, while wind pollination alone produced 49.5-51.2%, a smaller but substantial proportion of seed set with pollen supplementation. Further evidence for wind pollination was found in a comparison of sites differing in the extent of wind exposure in two populations of *L. parviflorus*. Airborne pollen counts were higher in exposed sites than in protected sites, and the difference was marginally significant. Seed set was significantly pollen limited in protected sites, but not in exposed sites. Taken together, the data suggest that wind pollination provides some reproductive assurance in this obligately outcrossing species. Wind pollination is hypothesized to represent an alternative to selfing as an evolutionary solution to the problem of temporal or spatial variation in pollination visitation.

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8/3,AB/58 (Item 51 from file: 98)  
DIALOG(F)File 98:General Sci Abs/Full-Text  
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04027875 H.W. WILSON RECORD NUMBER: BGSAA99027875  
Geographic distribution of molecular variance within the blue marlin (*Makaira nigricans*): a hierarchical analysis of allozyme, single-copy nuclear DNA, and mitochondrial DNA markers.

Bonacorsi, Vincent P  
Feege, Kimberly S; Morgan, Lee W  
Evolution (Evolution) v. 53 no2 (Apr. 1999) p. 568-79  
SPECIAL FEATURES: bibl il map ISSN: 0014-3820  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 9653

ABSTRACT: A comparative hierarchical analysis of variance applied to 3 classes of molecular markers within the blue marlin (*Makaira nigricans*) is described. Four polymorphic allozyme loci, 4 polymorphic anonymously chosen single copy nuclear DNA (scnDNA) loci, and previously reported restriction fragment length polymorphisms (RFLPs) of mitochondrial DNA (mtDNA) were

included in the study. Moderate levels of genetic variation were detected at both polymorphic allozyme and scnDNA loci. However, mtDNA markers showed much greater diversity. At 3 of 4 allozyme loci and 3 of 4 scnDNA loci, allele frequencies were significantly different between Atlantic and Pacific Ocean samples. Compared with divergence detected at nuclear loci, mtDNA RFLP divergence between oceans was significantly greater. The difference observed between nuclear and mitochondrial divergence estimates may be due to the 4-fold smaller effective population size of mtDNA and male-mediated gene flow

8/3,AB/59 (Item 52 from file: 98)  
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04027636 H.W. WILSON RECORD NUMBER: BGSAA99027636  
Integrating developmental evolutionary patterns and mechanisms: a case study using the gastropod radula.  
Guralnick, R. P  
Lindberg, D. R  
Evolution (Evolution) v. 53 no2 (Apr. 1999) p. 447-59  
SPECIAL FEATURES: bibl il ISSN: 0014-3820  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 10416

ABSTRACT: The patterns and processes of shape change in a model system, the gastropod radula, were examined. The gastropod radula possesses a simple system, having only 2 processes, initial selection and postsecretional movement of teeth. Taken together, the results of this study showed that 2 different ontogenetic processes can lead to similar expression of row shapes; therefore, phylogenetic homologies based on adult morphologies and ontogenetic process may be discordant.

8/3,AB/60 (Item 53 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04027633 H.W. WILSON RECORD NUMBER: BGSAA99027633  
Dynamic and genetic consequences of variation in horizontal transmission for a microparasitic infection.  
Schmid-Hempel, Paul  
Fuhr, Katina; Kruger, Nadja  
Evolution (Evolution) v. 53 no2 (Apr. 1999) p. 426-34  
SPECIAL FEATURES: bibl il ISSN: 0014-3820  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 7555

ABSTRACT: The way in which variation in the time to transmission and exposure to adverse conditions outside the host interact to determine the success of the infection in the next host was studied. This interaction was investigated using the trypanosome *Crithidia bombi* infecting its bumblebee host (*Bombus terrestris*). Overall, the findings show that the window of transmission was comparably less important than the transmission mode. Low host densities were seen to decrease the rate of contacts with new hosts and to decrease success because parasites had to wait longer at a transmission site.

8/3,AB/61 (Item 54 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04022237 H.W. WILSON RECORD NUMBER: BGS99022237  
Most unwanted: persistent organic pollutants.  
Fisher, Brandy E  
Environmental Health Perspectives (Environ Health Perspect) v. 107 nol  
(Jan. 1999) p. A18-A23  
SPECIAL FEATURES: il ISSN: 0091-6765  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 5434

ABSTRACT: A dozen chemicals have been identified by the UN Environmental Programme as powerful threats to human and wildlife health on a global basis. These chemicals belong to a class known as persistent organic pollutants, which are chemicals that can travel thousands of miles, accumulate in the food chain, and persist in the environment, taking up to centuries to fully degrade. Such compounds have been known to cause birth defects, various cancers, immune system dysfunction, and reproductive problems in wildlife. The 12 compounds are aldrin, chlordane, DDT, dieldrin, dioxins, endrin, furans, heptachlor, hexachlorobenzene, mirex, polychlorinated biphenyls, and toxaphene. The properties of these compounds, and some alternatives to them, are discussed.

8 '98, AB/62 (Item 55 from file: 98)  
DIALOG(R)File 98:General Sci Abs/Full-Text  
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04014874 H.W. WILSON RECORD NUMBER: BGS199014874  
The influence of population size and isolation on gene flow by pollen in  
Silene alba.  
Richards, Christopher M  
Church, Sheri; McCauley, David E  
Evolution (Evolution) v. 53 nol (Feb. 1999) p. 63-73  
SPECIAL FEATURES: bibl il ISSN: 0014-3820  
LANGUAGE: English  
COUNTRY OF PUBLICATION: United States  
WORD COUNT: 8643

ABSTRACT: The effects of flower number and distance between patches on gene flow by pollen in *Silene alba* were investigated. At 20 m, the mean immigration rate was just over 47 percent, whereas immigration rates were less than 6 percent at 80 m. The number of flowers in the focal and neighboring populations had a significant effect on the frequency of gene flow. Factors that influenced gene flow at one spatial scale did not act in the same way at another. The patterns of gene flow within a metapopulation system can be complex and may vary within a growing season.

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04014401 H.W. WILSON RECORD NUMBER: BGS199014401  
Heat-shock proteins, molecular chaperones, and the stress response:  
evolutionary and ecological physiology.  
AMENDED TITLE: review  
Feder, Martin E  
Hoffmann, Gretchen E  
Annual Review of Physiology (Annu Rev Physiol) v. 61 ('99) p. 243-82  
SPECIAL FEATURES: bibl il ISSN: 0066-4278  
LANGUAGE: English  
COUNTRY OF PUBLICATION United States  
WORD COUNT: 20648

ABSTRACT: Molecular chaperones, including the heat-shock proteins (Hsps), are a ubiquitous feature of cells in which these proteins cope with stress-induced denaturation of other proteins. Hsps have received the most attention in model organisms undergoing experimental stress in the laboratory, and the function of Hsps at the molecular and cellular level is becoming well understood in this context. A complementary focus is now emerging on the Hsps of both model and nonmodel organisms undergoing stress in nature, on the roles of Hsps in the stress physiology of whole multicellular eukaryotes and the tissues and organs they comprise, and on the ecological and evolutionary correlates of variation in Hsps and the genes that encode them. This focus discloses that (a) expression of Hsps can occur in nature, (b) all species have hsp genes but they vary in the patterns of their expression, (c) Hsp expression can be correlated with resistance to stress, and (d) species' thresholds for Hsp expression are correlated with levels of stress that they naturally undergo. These conclusions are now well established and may require little additional confirmation; many significant questions remain unanswered concerning both the mechanisms of Hsp-mediated stress tolerance at the organismal level and the evolutionary mechanisms that have diversified the hsp genes. With permission, from the Annual **Review** of Physiology, Volume 61, 1999, by Annual **Reviews** Inc. (<http://www.annurev.org> ).

8/3,AB/64 (Item 1 from file: 357)  
DIALOG(P) File 357:Derwent Biotech Res.  
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0269300 DBA Accession No.: 2001-08482  
Strategies for expressing multiple foreign genes in plants as polycistronic constructs - **vector**-mediated multiple transgene gene transfer and expression in transgenic plant for crop improvement, antibody, polymer or beta-carotene preparation; a **review**

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JOURNAL: In Vitro Cell.Dev.Biol.Plant (37, 3, 313-20) 2001  
ISSN: 1054-5476 CODEN: IVCPEO

LANGUAGE: English

ABSTRACT: Strategies for expressing multiple foreign genes in plants as polycistronic constructs are **reviewed**. There is an increased desire to express many foreign genes in the same transgenic plant. A range of approaches have been explored in the period since gene transfer was developed as a useful tool in plant science. These approaches have ranged from assembly of multiple transcription units on a single DNA **vector**, to the execution of several independent **transformations** involving single genes followed by successive rounds of hybridization to yield plant lines with the desired combination of genes, to cotransformation with multiple plasmids followed by molecular screening to identify desired transgenic plants. Recent developments have provided new alternatives to the problem of the expression of multiple transgenes in plants, approaches that are based on the expression of polycistronic mRNAs. Among the more exciting advances in recent years has been the use of multigene expression to produce transgenic plants capable of synthesizing antibodies, biodegradable polymers, and beta-carotenes in **rice** (*Oryza sativa*) endosperms. (54 ref)

8/3,AB/65 (Item 2 from file: 357)  
DIALOG(R) File 357:Derwent Biotech Res.  
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0262697 DBA Accession No.: 2001-02273

Production of agronomically superior transgenic **rice** plants using **Agrobacterium transformation** methods: present status and future perspectives - **Agrobacterium tumefaciens**-mediated gene transfer and expression in **rice** transgenic plant for crop improvement; a **review**

AUTHOR: Roy M; Jain R K; Fohila J S; Wu R

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JOURNAL: Curr.Sci. (79, 7, 954-60) 2000

ISSN: 0011-3891 CODEN: CUSCAM

LANGUAGE: English

ABSTRACT: The production of agronomically superior transgenic **rice** (*Oryza sativa*) plants using **Agrobacterium** sp. **transformation** methods and their present status and future perspectives are **reviewed**. **Agrobacterium tumefaciens** is a soil bacterium that can genetically **transform** plant cells by transferring defined piece of DNA (known as T-DNA) from its tumor-inducing (Ti) plasmid into the genome of infected plants. A large number of suitable **vectors** have been developed for **Agrobacterium** sp.-mediated **transformation**. This method also provides an opportunity to transfer large segments of DNA that may contain more than 10 genes without rearrangement, which are suitable for studying their cumulative, interactive effects on complex polygenic traits. This transfer method has given results of high-efficiency of **Agrobacterium**-mediated production of fertile and heritable transgenic **rice** plants. This technology has been adopted by many laboratories and is now in wide-spread use. This method of **transformation** has several advantages, including higher **transformation** efficiency, integration of relatively low number of transgene copies and low experimental costs. (76 ref)

8/3,AB/66 (Item 3 from file: 357)

DIALOG(R)File 357:Derwent Biotechn Res.

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0242611 DBA Accession No.: 1999-13566

Towards molecular farming in the future: using plant-cell-suspension cultures as bioreactors - for example **vector**-mediated tobacco transgenic plant construction, used for recombinant antibody, protein production, etc. **review**

AUTHOR: Fischer F; Emans N; Schnuter F; Hellwig S; Drossard J

CORPORATE AFFILIATE: Tech.Coll.Aachen-Inst.Biol.

Inst.Environ.Chem.Ecotox.Schmallenberg

CORPORATE SOURCE: Institut fuer Biologie, RWTH Aachen, Worringerweg 1, D-52074 Aachen, Germany.

JOURNAL: Biotechnol.Appl.Biochem. (30, Pt.2, 109-12) 1999

ISSN: 0935-4513 CODEN: BABIEC

LANGUAGE: English

ABSTRACT: Plant-suspension cells are **reviewed** as an in vitro system for the production of recombinant protein under carefully controlled conditions. Free cell suspensions are considered to be the most suitable for large-scale applications in the biotechnology industry. Plant species used for generation and propagation of suspension cell cultures include *Arabidopsis* sp., *Catharanthus* sp., yew (*Taxus* sp.), **rice** (*Oryza sativa*), soybean (*Glycine max*), alfalfa (*Medicago sativa*) and tobacco (*Nicotiana tabacum*). Plant cell suspensions can be cultivated in shake flasks or culture vessel using batch, fed batch, perfusion and continuous culture. For recombinant protein production **Agrobacterium** sp. mediated **transformation**,

microparticle bombardment, electroporation of protoplasts or virus **vectors** can all be used. Tobacco suspension cell cultures have been used to express IgGs, Fab fragments, single chains, bispecific antibody fragments and fusion proteins. Tobacco BY-2 cells have been used for culture using a working volume of 40 l. A 10% (v/v) inoculum with a culture time of 150 hr produced a yield of 7.5 kg fresh cell weight. (52 ref)

WORD COUNT: 22407

**ABSTRACT:** Retrotransposons are mobile genetic elements that transpose through reverse transcription of an RNA intermediate. Retrotransposons are ubiquitous in plants and play a major role in plant gene and genome evolution. In many cases, retrotransposons comprise over 50% of nuclear DNA content, a situation that can arise in just a few million years. Plant retrotransposons are structurally and functionally similar to the retrotransposons and retroviruses that are found in other eukaryotic organisms. However, there are important differences in the genomic organization of retrotransposons in plants compared to some other eukaryotes, including their often-high copy numbers, their extensively heterogeneous populations, and their chromosomal dispersion patterns. Recent studies are providing valuable insights into the mechanisms involved in regulating the expression and transposition of retrotransposons. This review describes the structure, genomic organization, expression, regulation, and evolution of retrotransposons, and discusses both their contributions to plant genome evolution and their use as genetic tools in plant biology. Reprinted by permission of the publisher.

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04255630 H.W. WILSON RECORD NUMBER: B3SA00005630  
Lentivirus replication and regulation.

DOCUMENT TYPE: **review**

Tang, Hengli

Kiken, Kelli L; Wong-Staal, Flossie

Annual Review of Genetics v. 33 (1999) p. 133-70

SPECIAL FEATURES: bibl il ISSN: 0066-4197

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 17942

**ABSTRACT:** Lentiviruses are associated with chronic diseases of the hematological and neurological systems in animals and man. In particular, human immunodeficiency virus type 1 (HIV-1) is the etiological agent of the global AIDS epidemic. The genomes of lentiviruses are complex, encoding a number of regulatory and accessory proteins not found in other retroviruses. This complexity is reflected in their replication cycle, which reveals intricate regulatory pathways and unique mechanisms for viral persistence. In this **review**, we highlight some of these unique features for HIV-1, with particular focus on the transcriptional and posttranscriptional control of gene expression. Although our understanding of the biology of HIV-1 is far from complete, the knowledge gained thus far has already led to novel strategies for both virus intervention and exploiting the lentiviruses for therapeutic applications. Reprinted by permission of the publisher.

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04255140 H.W. WILSON RECORD NUMBER: B3SA00005140

Phylogenetic structure in the grass family (Poaceae): evidence from the nuclear gene phytochrome B.

Mathews, Sarah

Tsai, Rocky C; Kellogg, Elizabeth A

American Journal of Botany v. 87 no. 1 Jan. 2000 p. 96-107

SPECIAL FEATURES: bibl il ISSN: 0002-9122

LANGUAGE: English